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(54) Title: α -AMYLASE MUTANTS		
(57) Abstract		
<p>The invention relates to a variant of a parent Termamyl-like α-amylase, which exhibits an alteration in at least one of the following properties relative to said parent α-amylase: i) improved pH stability at a pH from 8 to 10.5; and/or ii) improved Ca²⁺ stability at pH 8 to 10.5, and/or iii) increased specific activity at temperatures from 10 to 60 °C.</p>		

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α -amylase mutants

FIELD OF THE INVENTION

The present invention relates to variants (mutants) of parent
5 Termamyl-like α -amylases with higher activity at medium
temperatures and/or high pH.

BACKGROUND OF THE INVENTION

α -Amylases (α -1,4-glucan-4-glucanohydrolases, EC 3.2.1.1)
10 constitute a group of enzymes which catalyze hydrolysis of
starch and other linear and branched 1,4-glucosidic oligo- and
polysaccharides.

There is a very extensive body of patent and scientific
literature relating to this industrially very important class of
15 enzymes. A number of α -amylases such as Termamyl-like α -
amylases variants are known from e.g. WO 90/11352, WO 95/10603,
WO 95/26397, WO 96/23873 and WO 96/23874.

Among more recent disclosures relating to α -amylases, WO
96/23874 provides three-dimensional, X-ray crystal structural
20 data for a Termamyl-like α -amylase which consists of the 300 N-
terminal amino acid residues of the *B. amyloliquefaciens*
 α -amylase (BANTM) and amino acids 301-483 of the C-terminal end
of the *B. licheniformis* α -amylase comprising the amino acid
sequence (the latter being available commercially under the
25 tradename TermamylTM), and which is thus closely related to the
industrially important *Bacillus* α -amylases (which in the present
context are embraced within the meaning of the term "Termamyl-
like α -amylases", and which include, *inter alia*, the *B.*
licheniformis, *B. amyloliquefaciens* (BANTM) and *B.*
30 *stearothermophilus* (BSGTM) α -amylases). WO 96/23874 further
describes methodology for designing, on the basis of an analysis
of the structure of a parent Termamyl-like α -amylase, variants
of the parent Termamyl-like α -amylase which exhibit altered
properties relative to the parent.

BRIEF DISCLOSURE OF THE INVENTION

The present invention relates to novel α -amylolytic variants (mutants) of a Termamyl-like α -amylase which exhibit improved wash performance (relative to the parent α -amylase) at high pH and at a medium temperature.

The term "medium temperature" means in the context of the invention a temperature from 10°C to 60°C, preferably 20°C to 50°C, especially 30-40°C.

The term "high pH" means the alkaline pH which is today used for washing, more specifically from about pH 8 to 10.5.

In the context of the invention a "low temperature α -amylase" means an α -amylase which has a relative optimum activity in the temperature range from 0-30°C.

In the context of the invention a "medium temperature α -amylase" means an α -amylase which has an optimum activity in the temperature range from 30-60°C. For instance, SP690 and SP722 α -amylases, respectively, are "medium temperature α -amylases."

In the context of the invention a "high temperature α -amylase" is an α -amylase having the optimum activity in the temperature range from 60-110°C. For instance, Termamyl is a "high temperature α -amylase."

Alterations in properties which may be achieved in variants (mutants) of the invention are alterations in:

The stability of the Termamyl-like α -amylase at a pH from 8 to 10.5, and/or the Ca^{2+} stability at pH 8 to 10.5, and/or the specific activity at temperatures from 10 to 60°C, preferably 20-50°C, especially 30-40°C.

It should be noted that the relative temperature optimum is often dependent on the specific pH used. In other words the relative temperature optimum determined at, e.g. pH 8, may be substantially different from the relative temperature optimum determined at, e.g., pH 10.

The temperature's influence on the enzymatic activity

The dynamics in the active site and surroundings are dependent on the temperature and the amino acid composition and of strong importance for the relative temperature optimum of an enzyme. By comparing the dynamics of medium and high temperature α -amylases, regions of importance for the function of high temperature α -amylases at medium temperatures can be determined. The temperature activity profile of the SP722 α -amylase (SEQ ID NO: 2) and the *B. licheniformis* α -amylase (available from Novo Nordisk as Termamyl®) (SEQ ID NO: 4) are shown in Figure 2.

The relative temperature optimum of SP722 in absolute activities is shown to be higher at medium range temperatures (30-60°C) than the homologous *B. licheniformis* α -amylase, which has an optimum activity around 60-100°C. The profiles are mainly dependent on the temperature stability and the dynamics of the active site residues and their surroundings. Further, the activity profiles are dependent on the pH used and the pKa of the active site residues.

In the first aspect the invention relates to a variant of a parent Termamyl-like α -amylase, which variant has α -amylase activity, said variant comprises one or more mutations corresponding to the following mutations in the amino acid sequence shown in SEQ ID NO: 2:

T141, K142, F143, D144, F145, P146, G147, R148, G149,
Q174, R181, G182, D183, G184, K185, A186, W189, S193, N195,
H107, K108, G109, D166, W167, D168, Q169, S170, R171, Q172, F173,
F267, W268, K269, N270, D271, L272, G273, A274, L275, K311,
E346, K385, G456, N457, K458, P459, G460, T461, V462, T463.

A variant of the invention have one or more of the following substitutions or deletions:

T141A, D, R, N, C, E, Q, G, H, I, L, K, M, F, P, S, W, Y, V;
K142A, D, R, N, C, E, Q, G, H, I, L, M, F, P, S, T, W, Y, V;
F143A, D, R, N, C, E, Q, G, H, I, L, K, M, P, S, T, W, Y, V;
D144A, R, N, C, E, Q, G, H, I, L, K, M, F, P, S, T, W, Y, V;
F145A, D, R, N, C, E, Q, G, H, I, L, K, M, P, S, T, W, Y, V;
P146A, D, R, N, C, E, Q, G, H, I, L, K, M, F, S, T, W, Y, V;
G147A, D, R, N, C, E, Q, H, I, L, K, M, F, P, S, T, W, Y, V;

R148A, D, N, C, E, Q, G, H, I, L, K, M, F, P, S, T, W, Y, V;
G149A, D, R, N, C, E, Q, H, I, L, K, M, F, P, S, T, W, Y, V;
R181*, A, D, N, C, E, Q, G, H, I, L, K, M, F, P, S, T, W, Y, V;
G182*, A, D, R, N, C, E, Q, H, I, L, K, M, F, P, S, T, W, Y, V;
5 D183*, A, R, N, C, E, Q, G, H, I, L, K, M, F, P, S, T, W, Y, V;
G184*, A, R, D, N, C, E, Q, H, I, L, K, M, F, P, S, T, W, Y, V;
K185A, D, R, N, C, E, Q, G, H, I, L, M, F, P, S, T, W, Y, V;
A186D, R, N, C, E, Q, G, H, I, L, K, M, F, P, S, T, W, Y, V;
W189A, D, R, N, C, E, Q, G, H, I, L, K, M, F, P, S, T, Y, V;
10 S193A, D, R, N, C, E, Q, G, H, I, L, K, M, F, P, T, W, Y, V;
N195A, D, R, C, E, Q, G, H, I, L, K, M, F, P, S, T, W, Y, V;
H107A, D, R, N, C, E, Q, G, I, L, K, M, F, P, S, T, W, Y, V;
K108A, D, R, N, C, E, Q, G, H, I, L, M, F, P, S, T, W, Y, V;
G109A, D, R, N, C, E, Q, H, I, L, K, M, F, P, S, T, W, Y, V;
15 D166A, R, N, C, E, Q, G, H, I, L, K, M, F, P, S, T, W, Y, V;
W167A, D, R, N, C, E, Q, G, H, I, L, K, M, F, P, S, T, Y, V;
D168A, R, N, C, E, Q, G, H, I, L, K, M, F, P, S, T, W, Y, V;
Q169A, D, R, N, C, E, G, H, I, L, K, M, F, P, S, T, W, Y, V;
S170A, D, R, N, C, E, Q, G, H, I, L, K, M, F, P, T, W, Y, V;
20 R171A, D, N, C, E, Q, G, H, I, L, K, M, F, P, S, T, W, Y, V;
Q172A, D, R, N, C, E, G, H, I, L, K, M, F, P, S, T, W, Y, V;
F173A, D, R, N, C, E, Q, G, H, I, L, K, M, P, S, T, W, Y, V;
Q174*, A, D, R, N, C, E, G, H, I, L, K, M, F, P, S, T, W, Y, V;
F267A, D, R, N, C, E, Q, G, H, I, L, K, M, P, S, T, W, Y, V;
25 W268A, D, R, N, C, E, Q, G, H, I, L, K, M, F, P, S, T, Y, V;
K269A, D, R, N, C, E, Q, G, H, I, L, M, F, P, S, T, W, Y, V;
N270A, D, R, C, E, Q, G, H, I, L, K, M, F, P, S, T, W, Y, V;
D271A, R, N, C, E, Q, G, H, I, L, K, M, F, P, S, T, W, Y, V;
L272A, D, R, N, C, E, Q, G, H, I, K, M, F, P, S, T, W, Y, V;
30 G273A, D, R, N, C, E, Q, H, I, L, K, M, F, P, S, T, W, Y, V;
A274D, R, N, C, E, Q, G, H, I, L, K, M, F, P, S, T, W, Y, V;
L275A, D, R, N, C, E, Q, G, H, I, K, M, F, P, S, T, W, Y, V;
K311A, D, R, N, C, E, Q, G, H, I, L, M, F, P, S, T, W, Y, V;
E346A, D, R, N, C, Q, G, H, I, K, L, M, F, P, S, T, W, Y, V;
35 K385A, D, R, N, C, E, Q, G, H, I, L, M, F, P, S, T, W, Y, V;
G456A, D, R, N, C, E, Q, H, I, L, K, M, F, P, S, T, W, Y, V;
N457A, D, R, C, E, Q, G, H, I, L, K, M, F, P, S, T, W, Y, V;
K458A, D, R, N, C, E, Q, G, H, I, L, M, F, P, S, T, W, Y, V;

P459A,D,R,N,C,E,Q,G,H,I,L,K,M,F,S,T,W,Y,V;

G460A,D,R,N,C,E,Q,H,I,L,K,M,F,P,S,T,W,Y,V;

T461A,D,R,N,C,E,Q,G,H,I,L,K,M,F,P,S,W,Y,V;

V462A,D,R,N,C,E,Q,G,H,I,L,K,M,F,P,S,T,W,Y;

5 T463A,D,R,N,C,E,Q,G,H,I,L,K,M,F,P,S,W,Y,V.

Preferred are variants having one or more of the following substitutions or deletions:

K142R; S193P; N195F; K269R,Q; N270Y,R,D; K311R; E346Q; K385R;

K458R; P459T; T461P; Q174*; R181Q,N,S; G182T,S,N; D183*; G184*;

10 K185A,R,D,C,E,Q,G,H,I,L,M,N,F,P,S,T,W,Y,V;A186T,S,N,I,V,R;

189T,S,N,Q.

Especially preferred are variants having a deletion in positions D183 and G184 and further one or more of the following substitutions or deletions:

15 K142R; S193P; N195F; K269R,Q; N270Y,R,D; K311R; E346Q; K385R;

K458R; P459T; T461P; Q174*; R181Q,N,S; G182T,S,N;

K185A,R,D,C,E,Q,G,H,I,L,M,N,F,P,S,T,W,Y,V; A186T,S,N,I,V,R;

W189T,S,N,Q.

The variants of the invention mentioned above exhibits an alteration in at least one of the following properties relative to the parent α -amylase:

i) improved pH stability at a pH from 8 to 10.5; and/or

ii) improved Ca^{2+} stability at pH 8 to 10.5, and/or

iii) increased specific activity at temperatures from 10 to 60°C,

25 preferably 20-50°C, especially 30-40°C. Further, details will be described below.

The invention further relates to DNA constructs encoding variants of the invention; to methods for preparing variants of the invention; and to the use of variants of the invention, alone or in combination with other enzymes, in various industrial products or processes, e.g., in detergents or for starch liquefaction.

In a final aspect the invention relates to a method of providing α -amylases with altered pH optimum, and/or altered temperature optimum, and/or improved stability.

Nomenclature

In the present description and claims, the conventional one-

letter and three-letter codes for amino acid residues are used.

For ease of reference, α -amylase variants of the invention are described by use of the following nomenclature:

Original amino acid(s):position(s):substituted amino acid(s)

5 According to this nomenclature, for instance the substitution of alanine for asparagine in position 30 is shown as:

Ala30Asn or A30N

a deletion of alanine in the same position is shown as:

Ala30* or A30*

10 and insertion of an additional amino acid residue, such as lysine, is shown as:

Ala30AlaLys or A30AK

A deletion of a consecutive stretch of amino acid residues, such as amino acid residues 30-33, is indicated as (30-33)* or
15 Δ (A30-N33).

Where a specific α -amylase contains a "deletion" in comparison with other α -amylases and an insertion is made in such a position this is indicated as:

*36Asp or *36D

20 for insertion of an aspartic acid in position 36

Multiple mutations are separated by plus signs, i.e.:

Ala30Asp + Glu34Ser or A30N+E34S

representing mutations in positions 30 and 34 substituting alanine and glutamic acid for asparagine and serine,
25 respectively.

When one or more alternative amino acid residues may be inserted in a given position it is indicated as

A30N,E or

A30N or A30E

30 Furthermore, when a position suitable for modification is identified herein without any specific modification being suggested, it is to be understood that any amino acid residue may be substituted for the amino acid residue present in the position. Thus, for instance, when a modification of an alanine
35 in position 30 is mentioned, but not specified, it is to be understood that the alanine may be deleted or substituted for any other amino acid, i.e., any one of:

R,N,D,A,C,Q,E,G,H,I,L,K,M,F,P,S,T,W,Y,V.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 is an alignment of the amino acid sequences of six parent Termamyl-like α -amylases. The numbers on the extreme left designate the respective amino acid sequences as follows:

1: SEQ ID NO: 2

2: Kaoamyl

3: SEQ ID NO: 1

10 4: SEQ ID NO: 5

5: SEQ ID NO: 4

6: SEQ ID NO: 3.

Figure 2 shows the temperature activity profile of SP722 (SEQ ID NO: 2) (at pH 9) and *B. licheniformis* α -amylase (SEQ ID NO: 4) (at pH 7.3).

Figure 3 shows the temperature profile for SP690 (SEQ ID NO: 1), SP722 (SEQ ID NO: 2), *B. licheniformis* α -amylase (SEQ ID NO: 4) at pH 10.

Figure 4 is an alignment of the amino acid sequences of five α -amylases. The numbers on the extreme left designate the respective amino acid sequences as follows:

1: amyp_mouse

2: amyp_rat

3: amyp_pig porcine pancreatic alpha-amylase (PPA)

25 4: amyp_human

5: amy_altha *A. haloplanctis* alpha-amylase (AHA)

DETAILED DISCLOSURE OF THE INVENTION

The Termamyl-like α -amylase

It is well known that a number of α -amylases produced by *Bacillus* spp. are highly homologous on the amino acid level. For instance, the *B. licheniformis* α -amylase comprising the amino acid sequence shown in SEQ ID NO: 4 (commercially available as Termamyl™) has been found to be about 89% homologous with the *B. amyloliquefaciens* α -amylase comprising the amino acid sequence shown in SEQ ID NO: 5 and about 79% homologous with the *B.*

stearothermophilus α -amylase comprising the amino acid sequence shown in SEQ ID NO: 3. Further homologous α -amylases include an α -amylase derived from a strain of the *Bacillus* sp. NCIB 12289, NCIB 12512, NCIB 12513 or DSM 9375, all of which are described in detail in WO 95/26397, and the α -amylase described by Tsukamoto et al., Biochemical and Biophysical Research Communications, 151 (1988), pp. 25-31, (see SEQ ID NO: 6).

Still further homologous α -amylases include the α -amylase produced by the *B. licheniformis* strain described in EP 0252666 (ATCC 27811), and the α -amylases identified in WO 91/00353 and WO 94/18314. Other commercial Termamyl-like *B. licheniformis* α -amylases are comprised in the products Optitherm™ and Takatherm™ (available from Solvay), Maxamyl™ (available from Gist-brocades/Genencor), Spezym AA™ and Spezyme Delta AA™ (available from Genencor), and Keistase™ (available from Daiwa).

Because of the substantial homology found between these α -amylases, they are considered to belong to the same class of α -amylases, namely the class of "Termamyl-like α -amylases".

Accordingly, in the present context, the term "Termamyl-like α -amylase" is intended to indicate an α -amylase which, at the amino acid level, exhibits a substantial homology to Termamyl™, i.e., the *B. licheniformis* α -amylase having the amino acid sequence shown in SEQ ID NO:4 herein. In other words, all the following α -amylases which has the amino acid sequences shown in SEQ ID NOS: 1, 2, 3, 4, 5, 6, 7 or 8 herein, or the amino acid sequence shown in SEQ ID NO: 1 of WO 95/26397 (the same as the amino acid sequence shown as SEQ ID NO: 7 herein) or in SEQ ID NO: 2 of WO 95/26397 (the same as the amino acid sequence shown as SEQ ID NO: 8 herein) or in Tsukamoto et al., 1988, (which amino acid sequence is shown in SEQ ID NO: 6 herein) are considered to be "Termamyl-like α -amylase". Other Termamyl-like α -amylases are α -amylases i) which displays at least 60%, such as at least 70%, e.g., at least 75%, or at least 80%, e.g., at least 85%, at least 90% or at least 95% homology with at least

one of said amino acid sequences shown in SEQ ID NOS: 1-8 and/or ii) displays immunological cross-reactivity with an antibody raised against at least one of said α -amylases, and/or iii) is encoded by a DNA sequence which hybridizes to the DNA sequences encoding the above-specified α -amylases which are apparent from SEQ ID NOS: 9, 10, 11, or 12 of the present application (which encoding sequences encode the amino acid sequences shown in SEQ ID NOS: 1, 2, 3, 4 and 5 herein, respectively), from SEQ ID NO: 4 of WO 95/26397 (which DNA sequence, together with the stop codon TAA, is shown in SEQ ID NO: 13 herein and encodes the amino acid sequence shown in SEQ ID NO: 8 herein) and from SEQ ID NO: 5 of WO 95/26397 (shown in SEQ ID NO: 14 herein), respectively.

In connection with property i), the "homology" may be determined by use of any conventional algorithm, preferably by use of the GAP programme from the GCG package version 7.3 (June 1993) using default values for GAP penalties, which is a GAP creation penalty of 3.0 and GAP extension penalty of 0.1, (Genetic Computer Group (1991) Programme Manual for the GCG Package, version 7, 575 Science Drive, Madison, Wisconsin, USA 53711).

A structural alignment between Termamyl (SEQ ID NO: 4) and a Termamyl-like α -amylase may be used to identify equivalent/corresponding positions in other Termamyl-like α -amylases. One method of obtaining said structural alignment is to use the Pile Up programme from the GCG package using default values of gap penalties, i.e., a gap creation penalty of 3.0 and gap extension penalty of 0.1. Other structural alignment methods include the hydrophobic cluster analysis (Gaboriaud et al., (1987), FEBS LETTERS 224, pp. 149-155) and reverse threading (Huber, T ; Torda, AE, PROTEIN SCIENCE Vol. 7, No. 1 pp. 142-149 (1998)).

Property ii) of the α -amylase, i.e., the immunological cross reactivity, may be assayed using an antibody raised against, or reactive with, at least one epitope of the relevant Termamyl-like α -amylase. The antibody, which may either be monoclonal or polyclonal, may be produced by methods known in

the art, e.g., as described by Hudson et al., Practical Immunology, Third edition (1989), Blackwell Scientific Publications. The immunological cross-reactivity may be determined using assays known in the art, examples of which are Western Blotting or radial immunodiffusion assay, e.g., as described by Hudson et al., 1989. In this respect, immunological cross-reactivity between the α -amylases having the amino acid sequences SEQ ID NOS: 1, 2, 3, 4, 5, 6, 7, or 8, respectively, has been found.

The oligonucleotide probe used in the characterisation of the Termamyl-like α -amylase in accordance with property iii) above may suitably be prepared on the basis of the full or partial nucleotide or amino acid sequence of the α -amylase in question.

Suitable conditions for testing hybridisation involve pre-soaking in 5xSSC and prehybridizing for 1 hour at $\sim 40^{\circ}\text{C}$ in a solution of 20% formamide, 5xDenhardt's solution, 50mM sodium phosphate, pH 6.8, and 50mg of denatured sonicated calf thymus DNA, followed by hybridisation in the same solution supplemented with 100mM ATP for 18 hours at $\sim 40^{\circ}\text{C}$, followed by three times washing of the filter in 2xSSC, 0.2% SDS at 40°C for 30 minutes (low stringency), preferred at 50°C (medium stringency), more preferably at 65°C (high stringency), even more preferably at $\sim 75^{\circ}\text{C}$ (very high stringency). More details about the hybridisation method can be found in Sambrook et al., Molecular Cloning: A Laboratory Manual, 2nd Ed., Cold Spring Harbor, 1989.

In the present context, "derived from" is intended not only to indicate an α -amylase produced or producible by a strain of the organism in question, but also an α -amylase encoded by a DNA sequence isolated from such strain and produced in a host organism transformed with said DNA sequence. Finally, the term is intended to indicate an α -amylase which is encoded by a DNA sequence of synthetic and/or cDNA origin and which has the identifying characteristics of the α -amylase in question. The term is also intended to indicate that the parent α -amylase may be a variant of a naturally occurring α -amylase, i.e. a variant which is the result of a modification (insertion, substitution,

deletion) of one or more amino acid residues of the naturally occurring α -amylase.

Parent hybrid α -amylases

5 The parent α -amylase (i.e., backbone α -amylase) may be a hybrid α -amylase, i.e., an α -amylase which comprises a combination of partial amino acid sequences derived from at least two α -amylases.

10 The parent hybrid α -amylase may be one which on the basis of amino acid homology and/or immunological cross-reactivity and/or DNA hybridization (as defined above) can be determined to belong to the Termamyl-like α -amylase family. In this case, the hybrid α -amylase is typically composed of at least one part of a Termamyl-like α -amylase and part(s) of one or more other α -
15 amylases selected from Termamyl-like α -amylases or non-Termamyl-like α -amylases of microbial (bacterial or fungal) and/or mammalian origin.

Thus, the parent hybrid α -amylase may comprise a combination of partial amino acid sequences deriving from at least two
20 Termamyl-like α -amylases, or from at least one Termamyl-like and at least one non-Termamyl-like bacterial α -amylase, or from at least one Termamyl-like and at least one fungal α -amylase. The Termamyl-like α -amylase from which a partial amino acid sequence derives may, e.g., be any of those specific Termamyl-like α -
25 amylase referred to herein.

For instance, the parent α -amylase may comprise a C-terminal part of an α -amylase derived from a strain of *B. licheniformis*, and a N-terminal part of an α -amylase derived from a strain of *B. amyloliquefaciens* or from a strain of *B. stearrowthermophilus*.
30 For instance, the parent α -amylase may comprise at least 430 amino acid residues of the C-terminal part of the *B. licheniformis* α -amylase, and may, e.g., comprise a) an amino acid segment corresponding to the 37 N-terminal amino acid

residues of the *B. amyloliquefaciens* α -amylase having the amino acid sequence shown in SEQ ID NO: 5 and an amino acid segment corresponding to the 445 C-terminal amino acid residues of the *B. licheniformis* α -amylase having the amino acid sequence shown in SEQ ID NO: 4, or

a hybrid Termamyl-like α -amylase being identical to the Termamyl sequence, i.e., the *Bacillus licheniformis* α -amylase shown in SEQ ID NO: 4, except that the N-terminal 35 amino acid residues (of the mature protein) has been replaced by the N-terminal 33 residues of BAN (mature protein), i.e., the *Bacillus amyloliquefaciens* α -amylase shown in SEQ ID NO: 5; or

b) an amino acid segment corresponding to the 68 N-terminal amino acid residues of the *B. stearothermophilus* α -amylase having the amino acid sequence shown in SEQ ID NO: 3 and an amino acid segment corresponding to the 415 C-terminal amino acid residues of the *B. licheniformis* α -amylase having the amino acid sequence shown in SEQ ID NO: 4.

Another suitable parent hybrid α -amylase is the one previously described in WO 96/23874 (from Novo Nordisk) constituting the N-terminus of BAN, *Bacillus amyloliquefaciens* α -amylase (amino acids 1-300 of the mature protein) and the C-terminus from Termamyl (amino acids 301-483 of the mature protein). Increased activity was achieved by substituting one or more of the following positions of the above hybrid α -amylase (BAN:1-300/Termamyl:301-483): Q360, F290, and N102. Particularly interesting substitutions are one or more of the following substitutions: Q360E,D; F290A,C,D,E,G,H,I,K,L,M,N,P,Q,R,S,T; N102D,E;

The corresponding positions in the SP722 α -amylase shown in SEQ ID NO: 2 are one or more of: S365, Y295, N106. Corresponding substitutions of particular interest in said α -amylase shown in SEQ ID NO: 2 are one or more of: S365D,E; Y295 A,C,D,E,G,H,I,K,L,M,N,P,Q,R,S,T; and N106D,E.

The corresponding positions in the SP690 α -amylase shown in SEQ ID NO: 1 are one or more of: S365, Y295, N106. The

corresponding substitutions of particular interest are one or more of: S365D,E; Y295 A,C,D,E,G,H,I,K,L,M,N,P,Q,R,S,T; N106D,E.

The above mentioned non-Termamyl-like α -amylase may, e.g., be a fungal α -amylase, a mammalian or a plant α -amylase or a
5 bacterial α -amylase (different from a Termamyl-like α -amylase). Specific examples of such α -amylases include the *Aspergillus oryzae* TAKA α -amylase, the *A. niger* acid α -amylase, the *Bacillus subtilis* α -amylase, the porcine pancreatic α -amylase and a barley α -amylase. All of these α -amylases have elucidated
10 structures which are markedly different from the structure of a typical Termamyl-like α -amylase as referred to herein.

The fungal α -amylases mentioned above, i.e., derived from *A. niger* and *A. oryzae*, are highly homologous on the amino acid level and generally considered to belong to the same family of
15 α -amylases. The fungal α -amylase derived from *Aspergillus oryzae* is commercially available under the tradename Fungamyl™.

Furthermore, when a particular variant of a Termamyl-like α -amylase (variant of the invention) is referred to - in a conventional manner - by reference to modification (e.g.,
20 deletion or substitution) of specific amino acid residues in the amino acid sequence of a specific Termamyl-like α -amylase, it is to be understood that variants of another Termamyl-like α -amylase modified in the equivalent position(s) (as determined from the best possible amino acid sequence alignment between the
25 respective amino acid sequences) are encompassed thereby.

In a preferred embodiment of the invention the α -amylase backbone is derived from *B. licheniformis* (as the parent Termamyl-like α -amylase), e.g., one of those referred to above, such as the *B. licheniformis* α -amylase having the amino acid
30 sequence shown in SEQ ID NO: 4.

Altered properties of variants of the invention

The following discusses the relationship between mutations which are present in variants of the invention, and desirable

alterations in properties (relative to those a parent Termamyl-like α -amylase) which may result therefrom.

Improved stability at pH 8-10.5

5 In the context of the present invention, mutations (including amino acid substitutions) of importance with respect to achieving improved stability at high pH (*i.e.*, pH 8-10.5) include mutations corresponding to mutations in one or more of the following positions in SP722 α -amylase (having the amino
10 acid sequence shown in SEQ ID NO: 2): T141, K142, F143, D144, F145, P146, G147, R148, G149, R181, A186, S193, N195, K269, N270, K311, K458, P459, T461.

The variant of the invention have one or more of the following substitutions (using the SEQ ID NO: 2 numbering):

15 T141A, D, R, N, C, E, Q, G, H, I, L, K, M, F, P, S, W, Y, V;
K142A, D, R, N, C, E, Q, G, H, I, L, M, F, P, S, T, W, Y, V;
F143A, D, R, N, C, E, Q, G, H, I, L, K, M, P, S, T, W, Y, V;
D144A, R, N, C, E, Q, G, H, I, L, K, M, F, P, S, T, W, Y, V;
F145A, D, R, N, C, E, Q, G, H, I, L, K, M, P, S, T, W, Y, V;
20 P146A, D, R, N, C, E, Q, G, H, I, L, K, M, F, S, T, W, Y, V;
G147A, D, R, N, C, E, Q, H, I, L, K, M, F, P, S, T, W, Y, V;
R148A, D, N, C, E, Q, G, H, I, L, K, M, F, P, S, T, W, Y, V;
G149A, D, R, N, C, E, Q, H, I, L, K, M, F, P, S, T, W, Y, V;
K181A, D, R, N, C, E, Q, G, H, I, L, M, F, P, S, T, W, Y, V;
25 A186D, R, N, C, E, Q, G, H, I, L, P, K, M, F, S, T, W, Y, V;
S193A, D, R, N, C, E, Q, G, H, I, L, K, M, F, P, T, W, Y, V;
N195A, D, R, C, E, Q, G, H, I, L, K, M, F, P, S, T, W, Y, V;
K269A, D, R, N, C, E, Q, G, H, I, L, M, F, P, S, T, W, Y, V;
N270A, D, R, C, E, Q, G, H, I, L, K, M, F, P, S, T, W, Y, V;
30 K311A, D, R, N, C, E, Q, G, H, I, L, M, F, P, S, T, W, Y, V;
K458A, D, R, N, C, E, Q, G, H, I, L, M, F, P, S, T, W, Y, V;
P459A, D, R, N, C, E, Q, G, H, I, L, K, M, F, S, T, W, Y, V;
T461A, D, R, N, C, E, Q, G, H, I, L, K, M, F, P, S, W, Y, V.

Preferred high pH stability variants include one or more of
35 the following substitutions in the SP722 α -amylase (having the amino acid sequence shown in SEQ ID NO: 2):
K142R, R181S, A186T, S193P, N195F, K269R, N270Y, K311R, K458R, P459T and T461P.

In specific embodiments the *Bacillus* strain NCIB 12512 α -amylase having the sequence shown in SEQ ID NO: 1, or the *B. stearothermophilus* α -amylase having the sequence shown in SEQ ID NO: 3, or the *B. licheniformis* α -amylase having the sequence
5 shown in SEQ ID NO: 4, or the *B. amyloliquefaciens* α -amylase having the sequence shown in SEQ ID NO: 5 is used as the backbone, i.e., parent Termamyl-like α -amylase, for these mutations.

As can be seen from the alignment in Figure 1 the *B. stearothermophilus* α -amylase already has a Tyrosine at position
10 corresponding to N270 in SP722. Further, the *Bacillus* strain NCIB 12512 α -amylase, the *B. stearothermophilus* α -amylase, the *B. licheniformis* α -amylase and the *B. amyloliquefaciens* α -amylase already have Arginine at position corresponding to K458
15 in SP722. Furthermore, the *B. licheniformis* α -amylase already has a Proline at position corresponding to T461 in SP722. Therefore, for said α -amylases these substitutions are not relevant.

α -amylase variants with improved stability at high pH can be
20 constructed by making substitutions in the regions found using the molecular dynamics simulation mentioned in Example 2. The simulation depicts the region(s) that has a higher flexibility or mobility at high pH (i.e., pH 8-10.5) when compared to medium pH.

By using the structure of any bacterial alpha-amylase with
25 homology (as defined below) to the Termamyl-like α -amylase (BA2), of which the 3D structure is disclosed in Appendix 1 of WO 96/23874 (from Novo Nordisk), it is possible to modelbuild the structure of such alpha-amylase and to subject it to
30 molecular dynamics simulations. The homology of said bacterial α -amylase may be at least 60%, preferably be more than 70%, more preferably more than 80%, most preferably more than 90% homologous to the above mentioned Termamyl-like α -amylase (BA2), measured using the UWGCG GAP program from the GCG package
35 version 7.3 (June 1993) using default values for GAP penalties

[Genetic Computer Group (1991) Programme Manual for the GCG Package, version 7, 575 Science Drive, Madison, Wisconsin, USA 53711]. Substitution of the unfavorable residue for another would be applicable.

5

Improved Ca²⁺ stability at pH 8-10.5

Improved Ca²⁺ stability means the stability of the enzyme under Ca²⁺ depletion has been improved. In the context of the present invention, mutations (including amino acid
10 substitutions) of importance with respect to achieving improved Ca²⁺ stability at high pH include mutation or deletion in one or more positions corresponding to the following positions in the SP722 α -amylase having the amino acid sequence shown in SEQ ID NO: 2: R181, G182, D183, G184, K185, A186, W189, N195, N270,
15 E346, K385, K458, P459.

A variant of the invention have one or more of the following substitutions or deletions:

R181*, A, D, N, C, E, Q, G, H, I, L, K, M, F, P, S, T, W, Y, V;
G182*, A, D, R, N, C, E, Q, H, I, L, K, M, F, P, S, T, W, Y, V;
20 D183*, A, R, N, C, E, Q, G, H, I, L, K, M, F, P, S, T, W, Y, V;
G184*, A, R, D, N, C, E, Q, H, I, L, K, M, F, P, S, T, W, Y, V;
K185A, D, R, N, C, E, Q, G, H, I, L, M, F, P, S, T, W, Y, V;
A186D, R, N, C, E, Q, G, H, I, L, K, M, F, P, S, T, W, Y, V;
W189A, D, R, N, C, E, Q, G, H, I, L, K, M, F, P, S, T, Y, V;
25 N195A, D, R, C, E, Q, G, H, I, L, K, M, F, P, S, T, W, Y, V;
N270A, R, D, N, C, E, Q, H, I, L, K, M, F, P, S, T, W, Y, V;
E346A, R, D, N, C, Q, G, H, I, L, K, M, F, P, S, T, W, Y, V;
K385A, R, D, N, C, E, Q, G, H, I, L, M, F, P, S, T, W, Y, V;
K458A, R, D, N, C, E, Q, G, H, I, L, M, F, P, S, T, W, Y, V;
30 P459A, R, D, N, C, E, Q, G, H, I, L, K, M, F, S, T, W, Y, V.

Preferred are variants having one or more of the following substitutions or deletions:

R181Q, N; G182T, S, N; D183*; G184*;
K185A, R, D, C, E, Q, G, H, I, L, M, N, F, P, S, T, W, Y, V; A186T, S, N, I, V;
35 W189T, S, N, Q; N195F, N270R, D; E346Q; K385R; K458R; P459T.

In specific embodiments the *Bacillus* strain NCIB 12512 α -amylase having the sequence shown in SEQ ID NO: 1, or the *B. amyloliquefaciens* α -amylase having the sequence shown in SEQ ID

NO: 5, or the *B. licheniformis* α -amylase having the sequence shown in SEQ ID NO: 4 are used as the backbone for these mutations.

As can be seen from the alignment in Figure 1 the *B. licheniformis* α -amylase does not have the positions corresponding to D183 and G184 in SP722. Therefore for said α -amylases these deletions are not relevant.

In a preferred embodiment the variant is the *Bacillus* strain NCIB 12512 α -amylase with deletions in D183 and G184 and further one of the following substitutions: R181Q,N and/or G182T,S,N and/or D183*; G184* and/or K185A,R,D,C,E,Q,G,H,I,L,M,N,F,P,S,T,W,Y,V and/or A186T,S,N,I,V and/or W189T,S,N,Q and/or N195F and/or N270R,D and/or E346Q and/or K385R and/or K458R and/or P459T.

15

Increased specific activity at medium temperature

In a further aspect of the present invention, important mutations with respect to obtaining variants exhibiting increased specific activity at temperatures from 10-60°C, preferably 20-50°C, especially 30-40°C, include mutations corresponding to one or more of the following positions in the SP722 α -amylase having the amino acid sequence shown in SEQ ID NO: 2:

H107, K108, G109, D166, W167, D168, Q169, S170, R171, Q172, F173, Q174, D183, G184, N195, F267, W268, K269, N270, D271, L272, G273, A274, L275, G456, N457, K458, P459, G460, T461, V462, T463.

The variant of the invention have one or more of the following substitutions:

H107A,D,R,N,C,E,Q,G,I,L,K,M,F,P,S,T,W,Y,V;
K108A,D,R,N,C,E,Q,G,H,I,L,M,F,P,S,T,W,Y,V;
G109A,D,R,N,C,E,Q,H,I,L,K,M,F,P,S,T,W,Y,V;
D166A,R,N,C,E,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V;
W167A,D,R,N,C,E,Q,G,H,I,L,K,M,F,P,S,T,Y,V;
D168A,R,N,C,E,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V;
Q169A,D,R,N,C,E,G,H,I,L,K,M,F,P,S,T,W,Y,V;

S170A, D, R, N, C, E, Q, G, H, I, L, K, M, F, P, T, W, Y, V;
 R171A, D, N, C, E, Q, G, H, I, L, K, M, F, P, S, T, W, Y, V;
 Q172A, D, R, N, C, E, G, H, I, L, K, M, F, P, S, T, W, Y, V;
 F173A, D, R, N, C, E, Q, G, H, I, L, K, M, P, S, T, W, Y, V;
 5 Q174*, A, D, R, N, C, E, G, H, I, L, K, M, F, P, S, T, W, Y, V;
 D183*, A, D, R, N, C, E, Q, G, H, I, L, K, M, F, P, S, W, Y, V;
 G184*, A, R, N, C, E, Q, G, H, I, L, K, M, F, P, S, T, W, Y, V;
 N195A, D, R, C, E, Q, G, H, I, L, K, M, F, P, S, T, W, Y, V;
 F267A, D, R, N, C, E, Q, G, H, I, L, K, M, P, S, T, W, Y, V;
 10 W268A, D, R, N, C, E, Q, G, H, I, L, K, M, F, P, S, T, Y, V;
 K269A, D, R, N, C, E, Q, G, H, I, L, M, F, P, S, T, W, Y, V;
 N270A, D, R, C, E, Q, G, H, I, L, K, M, F, P, S, T, W, Y, V;
 D271A, R, N, C, E, Q, G, H, I, L, K, M, F, P, S, T, W, Y, V;
 L272A, D, R, N, C, E, Q, G, H, I, K, M, F, P, S, T, W, Y, V;
 15 G273A, D, R, N, C, E, Q, H, I, L, K, M, F, P, S, T, W, Y, V;
 A274D, R, N, C, E, Q, G, H, I, L, K, M, F, P, S, T, W, Y, V;
 L275A, D, R, N, C, E, Q, G, H, I, K, M, F, P, S, T, W, Y, V;
 G456A, D, R, N, C, E, Q, H, I, L, K, M, F, P, S, T, W, Y, V;
 N457A, D, R, C, E, Q, G, H, I, L, K, M, F, P, S, T, W, Y, V;
 20 K458A, D, R, N, C, E, Q, G, H, I, L, M, F, P, S, T, W, Y, V;
 P459A, D, R, N, C, E, Q, G, H, I, L, K, M, F, S, T, W, Y, V;
 G460A, D, R, N, C, E, Q, H, I, L, K, M, F, P, S, T, W, Y, V;
 T461A, D, R, N, C, E, Q, G, H, I, L, K, M, F, P, S, W, Y, V;
 V462A, D, R, N, C, E, Q, G, H, I, L, K, M, F, P, S, T, W, Y;
 25 T463A, D, R, N, C, E, Q, G, H, I, L, K, M, F, P, S, W, Y, V.

Preferred variants has one or more of the following substitutions or deletions: Q174*, D183*, G184*, K269S.

In a specific embodiment the *B. licheniformis* α -amylase having the sequence shown in SEQ ID NO: 4 is used as the
 30 backbone for these mutations.

General mutations in variants of the invention: increased specific activity at medium temperatures

The particularly interesting amino acid substitution are
 35 those that increase the mobility around the active site of the enzyme. This is accomplished by changes that disrupt stabilizing interaction in the vicinity of the active site, i.e., within preferably 10Å or 8Å or 6Å or 4Å from any of the residues

constituting the active site.

Examples are mutations that reduce the size of side chains, such as

Ala to Gly,

5 Val to Ala or Gly,

Ile or Leu to Val, Ala, or Gly

Thr to Ser

Such mutations are expected to cause increased flexibility in the active site region either by the introduction of cavities
10 or by the structural rearrangements that fill the space left by the mutation.

It may be preferred that a variant of the invention comprises one or more modifications in addition to those outlined above. Thus, it may be advantageous that one or more Proline residues
15 present in the part of the α -amylase variant which is modified is/are replaced with a non-Proline residue which may be any of the possible, naturally occurring non-Proline residues, and which preferably is an Alanine, Glycine, Serine, Threonine, Valine or Leucine.

20 Analogously, it may be preferred that one or more Cysteine residues present among the amino acid residues with which the parent α -amylase is modified is/are replaced with a non-Cysteine residue such as Serine, Alanine, Threonine, Glycine, Valine or Leucine.

25 Furthermore, a variant of the invention may - either as the only modification or in combination with any of the above outlined modifications - be modified so that one or more Asp and/or Glu present in an amino acid fragment corresponding to the amino acid fragment 185-209 of SEQ ID NO: 4 is replaced by
30 an Asn and/or Gln, respectively. Also of interest is the replacement, in the Termamyl-like α -amylase, of one or more of the Lys residues present in an amino acid fragment corresponding to the amino acid fragment 185-209 of SEQ ID NO: 4 by an Arg.

It will be understood that the present invention encompasses
35 variants incorporating two or more of the above outlined modifications.

Furthermore, it may be advantageous to introduce point-mutations in any of the variants described herein.

α -amylase variants having increased mobility around the active site:

The mobility of α -amylase variants of the invention may be increased by replacing one or more amino acid residue at one or more positions close to the substrate site. These positions are (using the SP722 α -amylase (SEQ ID NO: 2) numbering): V56, K108, D168, Q169, Q172, L201, K269, L272, L275, K446, P459.

Therefore, in an aspect the invention relates to variants being mutated in one or more of the above mentioned positions.

Preferred substitutions are one or more of the following:

V56A,G,S,T;

K108A,D,E,Q,G,H,I,L,M,N,S,T,V;

D168A,G,I,V,N,S,T;

15 Q169A,D,G,H,I,L,M,N,S,T,V;

Q172A,D,G,H,I,L,M,N,S,T,V;

L201A,G,I,V,S,T;

K269A,D,E,Q,G,H,I,L,M,N,S,T,V;

L272A,G,I,V,S,T;

20 L275A,G,I,V,S,T;

Y295A,D,E,Q,G,H,I,L,M,N,F,S,T,V;

K446A,D,E,Q,G,H,I,L,M,N,S,T,V;

P459A,G,I,L,S,T,V.

In specific embodiments of the invention the *Bacillus* strain NCIB 12512 α -amylase having the sequence shown in SEQ ID NO: 1, or the *B. stearothermophilus* α -amylase having the sequence shown in SEQ ID NO: 3, or the *B. licheniformis* α -amylase having the sequence shown in SEQ ID NO: 4, or the *B. amyloliquefaciens* α -amylase having the sequence shown in SEQ ID NO: 5 are used as the backbone for these mutations.

As can be seen from the alignment in Figure 1 the *B. licheniformis* α -amylase and the *B. amyloliquefaciens* α -amylase have a Glutamine at position corresponding to K269 in SP722. Further, the *B. stearothermophilus* α -amylase has a Serine at position corresponding to K269 in SP722. Therefore, for said α -amylases these substitutions are not relevant.

Furthermore, as can be seen from the alignment in Figure 1

the *B. amyloliquefaciens* α -amylase has an Alanine at position corresponding to L272 in SP722, and the *B. stearothermophilus* α -amylase has a Isoleucine at the position corresponding to L272 in SP722. Therefore, for said α -amylases these substitutions are not relevant.

As can be seen from the alignment in Figure 1, the *Bacillus* strain 12512 α -amylase has a Isoleucine at position corresponding to L275 in SP722. Therefore for said α -amylase this substitution is not relevant.

As can be seen from the alignment in Figure 1 the *B. amyloliquefaciens* α -amylase has a Phenylalanine at position corresponding to Y295 in SP722. Further, the *B. stearothermophilus* α -amylase has an Asparagine at position corresponding to Y295 in SP722. Therefore, for said α -amylases these substitutions are not relevant.

As can be seen from the alignment in Figure 1 the *B. licheniformis* α -amylase and the *B. amyloliquefaciens* α -amylase have a Asparagine at position corresponding to K446 in SP722. Further, the *B. stearothermophilus* α -amylase has a Histidine at position corresponding to K446 in SP722. Therefore, for said α -amylases these substitutions are not relevant.

As can be seen from the alignment in Figure 1 the *B. licheniformis* α -amylase, the *B. amyloliquefaciens* α -amylase and the *B. stearothermophilus* α -amylase have a Serine at position corresponding to P459 in SP722. Further, the *Bacillus* strain 12512 α -amylase has a Threonine at position corresponding to P459 in SP722. Therefore, for said α -amylases these substitutions are not relevant.

Stabilization of enzymes having high activity at medium temperatures

In a further embodiment the invention relates to improving the stability of low temperature α -amylases (e.g., *Alteromonas haloplanctis* (Feller et al., (1994), Eur. J. Biochem 222:441-447), and medium temperature α -amylases (e.g., SP722 and SP690) possessing medium temperature activity, i.e., commonly known as psychrophilic enzymes and mesophilic enzymes. The stability can

for this particular enzyme class be understood either as thermostability or the stability at Calcium depletion conditions.

Typically, enzymes displaying the high activity at medium temperatures also display severe problems under conditions that stress the enzyme, such as temperature or Calcium depletion.

Consequently, the objective is to provide enzymes that at the same time display the desired high activity at medium temperatures without loosing their activity under slightly stressed conditions.

The activity of the stabilized variant measured at medium temperatures should preferably be between 100% or more and 50%, and more preferably between 100% or more and 70%, and most preferably between 100% or more and 85% of the original activity at that specific temperature before stabilization of the enzyme and the resulting enzyme should withstand longer incubation at stressed condition than the wild type enzyme.

Contemplated enzymes include α -amylases of, e.g., bacterial or fungal origin.

An example of such a low temperature α -amylase is the one isolated from *Alteromonas haloplanctis* (Feller et al., (1994), Eur. J. Biochem 222:441-447). The crystal structure of this alpha-amylase has been solved (Aghajari et al., (1998), Protein Science 7:564-572).

The *A. haloplanctis* alpha-amylase (5 in alignment shown in Fig. 4) has a homology of approximately 66% to porcine pancreatic alpha-amylase (PPA) (3 in the alignment shown in Fig. 4). The PPA 3D structure is known, and can be obtained from Brookhaven database under the name 1OSE or 1DHK. Based on the homology to other more stable alpha amylases, stabilization of "the low temperature highly active enzyme" from *Alteromonas haloplanctis* alpha-amylase, can be obtained and at the same time retaining the desired high activity at medium temperatures.

Figure 4 shown a multiple sequence alignments of five α -amylases, including the AHA and the PPA α -amylase. Specific mutations giving increased stability in *Alteromonas haloplanctis* alpha-amylase:

T66P, Q69P, R155P, Q177R, A205P, A232P, L243R, V295P, S315R.

Methods for preparing α -amylase variants

Several methods for introducing mutations into genes are known in the art. After a brief discussion of the cloning of α -amylase-encoding DNA sequences, methods for generating mutations at specific sites within the α -amylase-encoding sequence will be discussed.

Cloning a DNA sequence encoding an α -amylase

The DNA sequence encoding a parent α -amylase may be isolated from any cell or microorganism producing the α -amylase in question, using various methods well known in the art. First, a genomic DNA and/or cDNA library should be constructed using chromosomal DNA or messenger RNA from the organism that produces the α -amylase to be studied. Then, if the amino acid sequence of the α -amylase is known, homologous, labeled oligonucleotide probes may be synthesized and used to identify α -amylase-encoding clones from a genomic library prepared from the organism in question. Alternatively, a labeled oligonucleotide probe containing sequences homologous to a known α -amylase gene could be used as a probe to identify α -amylase-encoding clones, using hybridization and washing conditions of lower stringency.

Yet another method for identifying α -amylase-encoding clones would involve inserting fragments of genomic DNA into an expression vector, such as a plasmid, transforming α -amylase-negative bacteria with the resulting genomic DNA library, and then plating the transformed bacteria onto agar containing a substrate for α -amylase, thereby allowing clones expressing the α -amylase to be identified.

Alternatively, the DNA sequence encoding the enzyme may be prepared synthetically by established standard methods, e.g., the phosphoroamidite method described by S.L. Beaucage and M.H. Caruthers (1981) or the method described by Matthes et al. (1984). In the phosphoroamidite method, oligonucleotides are synthesized, e.g., in an automatic DNA synthesizer, purified, annealed, ligated and cloned in appropriate vectors.

Finally, the DNA sequence may be of mixed genomic and synthetic origin, mixed synthetic and cDNA origin or mixed genomic and cDNA origin, prepared by ligating fragments of synthetic, genomic or cDNA origin (as appropriate, the fragments corresponding to various parts of the entire DNA sequence), in accordance with standard techniques. The DNA sequence may also be prepared by polymerase chain reaction (PCR) using specific primers, for instance as described in US 4,683,202 or R.K. Saiki et al. (1988).

Expression of α -amylase variants

According to the invention, a DNA sequence encoding the variant produced by methods described above, or by any alternative methods known in the art, can be expressed, in enzyme form, using an expression vector which typically includes control sequences encoding a promoter, operator, ribosome binding site, translation initiation signal, and, optionally, a repressor gene or various activator genes.

The recombinant expression vector carrying the DNA sequence encoding an α -amylase variant of the invention may be any vector which may conveniently be subjected to recombinant DNA procedures, and the choice of vector will often depend on the host cell into which it is to be introduced. Thus, the vector may be an autonomously replicating vector, i.e., a vector which exists as an extrachromosomal entity, the replication of which is independent of chromosomal replication, e.g., a plasmid, a bacteriophage or an extrachromosomal element, minichromosome or an artificial chromosome. Alternatively, the vector may be one which, when introduced into a host cell, is integrated into the host cell genome and replicated together with the chromosome(s) into which it has been integrated.

In the vector, the DNA sequence should be operably connected to a suitable promoter sequence. The promoter may be any DNA sequence which shows transcriptional activity in the host cell of choice and may be derived from genes encoding proteins either homologous or heterologous to the host cell. Examples of suitable promoters for directing the transcription of the DNA sequence encoding an α -amylase variant of the invention,

sequence which shows transcriptional activity in the host cell of choice and may be derived from genes encoding proteins either homologous or heterologous to the host cell. Examples of suitable promoters for directing the transcription of the DNA sequence encoding an α -amylase variant of the invention, especially in a bacterial host, are the promoter of the *lac* operon of *E.coli*, the *Streptomyces coelicolor* agarase gene *dagA* promoters, the promoters of the *Bacillus licheniformis* α -amylase gene (*amyL*), the promoters of the *Bacillus stearothermophilus* maltogenic amylase gene (*amyM*), the promoters of the *Bacillus amyloliquefaciens* α -amylase (*amyQ*), the promoters of the *Bacillus subtilis* *xylA* and *xylB* genes etc. For transcription in a fungal host, examples of useful promoters are those derived from the gene encoding *A. oryzae* TAKA amylase, *Rhizomucor miehei* aspartic proteinase, *A. niger* neutral α -amylase, *A. niger* acid stable α -amylase, *A. niger* glucoamylase, *Rhizomucor miehei* lipase, *A. oryzae* alkaline protease, *A. oryzae* triose phosphate isomerase or *A. nidulans* acetamidase.

The expression vector of the invention may also comprise a suitable transcription terminator and, in eukaryotes, polyadenylation sequences operably connected to the DNA sequence encoding the α -amylase variant of the invention. Termination and polyadenylation sequences may suitably be derived from the same sources as the promoter.

The vector may further comprise a DNA sequence enabling the vector to replicate in the host cell in question. Examples of such sequences are the origins of replication of plasmids pUC19, pACYC177, pUB110, pE194, pAMB1 and pIJ702.

The vector may also comprise a selectable marker, e.g. a gene the product of which complements a defect in the host cell, such as the *dal* genes from *B. subtilis* or *B. licheniformis*, or one which confers antibiotic resistance such as ampicillin, kanamycin, chloramphenicol or tetracyclin resistance. Furthermore, the vector may comprise *Aspergillus* selection markers such as *amdS*, *argB*, *niaD* and *sC*, a marker giving rise to hygromycin resistance, or the selection may be accomplished by co-transformation, e.g., as described in WO 91/17243.

While intracellular expression may be advantageous in some respects, e.g., when using certain bacteria as host cells, it is generally preferred that the expression is extracellular. In general, the *Bacillus* α -amylases mentioned herein comprise a preregion permitting secretion of the expressed protease into the culture medium. If desirable, this preregion may be replaced by a different preregion or signal sequence, conveniently accomplished by substitution of the DNA sequences encoding the respective preregions.

The procedures used to ligate the DNA construct of the invention encoding an α -amylase variant, the promoter, terminator and other elements, respectively, and to insert them into suitable vectors containing the information necessary for replication, are well known to persons skilled in the art (cf., for instance, Sambrook et al., Molecular Cloning: A Laboratory Manual, 2nd Ed., Cold Spring Harbor, 1989).

The cell of the invention, either comprising a DNA construct or an expression vector of the invention as defined above, is advantageously used as a host cell in the recombinant production of an α -amylase variant of the invention. The cell may be transformed with the DNA construct of the invention encoding the variant, conveniently by integrating the DNA construct (in one or more copies) in the host chromosome. This integration is generally considered to be an advantage as the DNA sequence is more likely to be stably maintained in the cell. Integration of the DNA constructs into the host chromosome may be performed according to conventional methods, e.g., by homologous or heterologous recombination. Alternatively, the cell may be transformed with an expression vector as described above in connection with the different types of host cells.

The cell of the invention may be a cell of a higher organism such as a mammal or an insect, but is preferably a microbial cell, e.g. a bacterial or a fungal (including yeast) cell.

Examples of suitable bacteria are Gram positive bacteria such as *Bacillus subtilis*, *Bacillus licheniformis*, *Bacillus lentus*, *Bacillus brevis*, *Bacillus stearothermophilus*, *Bacillus alkalo-*
philus, *Bacillus amyloliquefaciens*, *Bacillus coagulans*, *Bacillus circulans*, *Bacillus lautus*, *Bacillus megaterium*, *Bacillus*

thuringiensis, or *Streptomyces lividans* or *Streptomyces murinus*, or gramnegative bacteria such as *E.coli*. The transformation of the bacteria may, for instance, be effected by protoplast transformation or by using competent cells in a manner known *per se*.

5 The yeast organism may favorably be selected from a species of *Saccharomyces* or *Schizosaccharomyces*, e.g. *Saccharomyces cerevisiae*. The filamentous fungus may advantageously belong to a species of *Aspergillus*, e.g., *Aspergillus oryzae* or *Aspergillus niger*. Fungal cells may be transformed by a process involving
10 protoplast formation and transformation of the protoplasts followed by regeneration of the cell wall in a manner known *per se*. A suitable procedure for transformation of *Aspergillus* host cells is described in EP 238 023.

In a yet further aspect, the present invention relates to a
15 method of producing an α -amylase variant of the invention, which method comprises cultivating a host cell as described above under conditions conducive to the production of the variant and recovering the variant from the cells and/or culture medium.

The medium used to cultivate the cells may be any conventional
20 medium suitable for growing the host cell in question and obtaining expression of the α -amylase variant of the invention. Suitable media are available from commercial suppliers or may be prepared according to published recipes (e.g. as described in catalogues of the American Type Culture Collection).

25 The α -amylase variant secreted from the host cells may conveniently be recovered from the culture medium by well-known procedures, including separating the cells from the medium by centrifugation or filtration, and precipitating proteinaceous components of the medium by means of a salt such as ammonium
30 sulphate, followed by the use of chromatographic procedures such as ion exchange chromatography, affinity chromatography, or the like.

Industrial Applications

35 The α -amylase variants of this invention possesses valuable properties allowing for a variety of industrial applications. In particular, enzyme variants of the invention are applicable as a component in washing, dishwashing and hard-surface cleaning

detergent compositions.

Numerous variants are particularly useful in the production of sweeteners and ethanol from starch, and/or for textile desizing. Conditions for conventional starch- conversion processes, including starch liquefaction and/or saccharification processes, are described in, e.g., US 3,912,590 and in EP patent publications Nos. 252,730 and 63,909.

Detergent compositions

As mentioned above, variants of the invention may suitably be incorporated in detergent compositions. Reference is made, for example, to WO 96/23874 and WO 97/07202 for further details concerning relevant ingredients of detergent compositions (such as laundry or dishwashing detergents), appropriate methods of formulating the variants in such detergent compositions, and for examples of relevant types of detergent compositions.

Detergent compositions comprising a variant of the invention may additionally comprise one or more other enzymes, such as a lipase, cutinase, protease, cellulase, peroxidase or laccase, and/or another α -amylase.

α -amylase variants of the invention may be incorporated in detergents at conventionally employed concentrations. It is at present contemplated that a variant of the invention may be incorporated in an amount corresponding to 0.00001-1 mg (calculated as pure, active enzyme protein) of α -amylase per liter of wash/dishwash liquor using conventional dosing levels of detergent.

The invention also relates to a method of providing α -amylases with 1) altered pH optimum, and/or 2) altered temperature optimum, and/or 3) improved stability, comprising the following steps:

- i) identifying (a) target position(s) and/or region(s) for mutation of the α -amylase by comparing the molecular dynamics of two or more α -amylase 3D structures having substantially different pH, temperature and/or stability profiles,
- ii) substituting, adding and/or deleting one or more amino acids in the identified position(s) and/or region(s).

In embodiment of the invention a medium temperature α -amylase is compared with a high temperature α -amylase. In another embodiment a low temperature α -amylase is compared with either a medium or a high temperature α -amylase.

5 The α -amylases compared should preferably be at least 70%, preferably 80%, up to 90%, such as up to 95%, especially 95% homologous with each other.

The α -amylases compared may be Termamyl-like α -amylases as defined above. In specific embodiment the α -amylases compared
10 are the α -amylases shown in SEQ ID NO: 1 to SEQ ID NO: 8.

In another embodiment the stability profile of the α -amylases in question compared are the Ca^{2+} dependency profile.

MATERIALS AND METHODS

15 Enzymes:

SP722: (SEQ ID NO: 2, available from Novo Nordisk)

TermamylTM (SEQ ID NO: 4, available from Novo Nordisk)

SP690: (SEQ ID NO: 1, available from Novo Nordisk)

20 *Bacillus subtilis* SHA273: see WO 95/10603

Plasmids

pJE1 contains the gene encoding a variant of SP722 α -amylase (SEQ ID NO: 2): viz. deletion of 6 nucleotides corresponding to
25 amino acids D183-G184 in the mature protein. Transcription of the JE1 gene is directed from the *amyL* promoter. The plasmid further more contains the origin of replication and *cat*-gene conferring resistance towards kanamycin obtained from plasmid pUB110 (Gryczan, TJ et al. (1978), J. Bact. 134:318-329).

30

Methods:

Construction of library vector pDorK101

The *E. coli*/*Bacillus* shuttle vector pDorK101 (described below) can be used to introduce mutations without expression of
35 α -amylase in *E. coli* and then be modified in such way that the α -amylase is active in *Bacillus*. The vector was constructed as

follows: The JE1 encoding gene (SP722 with the deletion of D183-G184) was inactivated in pJE1 by gene interruption in the PstI site in the 5' coding region of the SEQ ID NO: 2: SP722 by a 1.2 kb fragment containing an *E. coli* origin of replication.

5 This fragment was PCR amplified from the pUC19 (GenBank Accession #:X02514) using the forward primer: 5'-gacctgcagtcaggcaacta-3' and the reverse primer: 5'-tagagtcgacctgcaggcat-3'. The PCR amplicon and the pJE1 vector were digested with PstI at 37°C for 2 hours. The pJE1 vector
10 fragment and the PCR fragment were ligated at room temperature for 1 hour and transformed in *E. coli* by electrotransformation. The resulting vector is designated pDorK101.

Filter screening assays

15 The assay can be used to screening of Termamyl-like α -amylase variants having an improved stability at high pH compared to the parent enzyme and Termamyl-like α -amylase variants having an improved stability at high pH and medium temperatures compared to the parent enzyme depending of the
20 screening temperature setting

High pH filter assay

Bacillus libraries are plated on a sandwich of cellulose acetate (OE 67, Schleicher & Schuell, Dassel, Germany) - and
25 nitrocellulose filters (Protran-Ba 85, Schleicher & Schuell, Dassel, Germany) on TY agar plates with 10 μ g/ml kanamycin at 37°C for at least 21 hours. The cellulose acetate layer is located on the TY agar plate.

Each filter sandwich is specifically marked with a needle
30 after plating, but before incubation in order to be able to localize positive variants on the filter and the nitrocellulose filter with bound variants is transferred to a container with glycine-NaOH buffer, pH 8.6-10.6 and incubated at room temperature (can be altered from 10°-60°C) for 15 min. The
35 cellulose acetate filters with colonies are stored on the TY-plates at room temperature until use. After incubation, residual activity is detected on plates containing 1% agarose,

0.2% starch in glycin-NaOH buffer, pH 8.6-10.6. The assay plates with nitrocellulose filters are marked the same way as the filter sandwich and incubated for 2 hours. at room temperature. After removal of the filters the assay plates are
5 stained with 10% Lugol solution. Starch degrading variants are detected as white spots on dark blue background and then identified on the storage plates. Positive variants are rescreened twice under the same conditions as the first screen.

10 Low calcium filter assay

The *Bacillus* library are plated on a sandwich of cellulose acetate (OE 67, Schleicher & Schuell, Dassel, Germany) - and nitrocellulose filters (Protran-Ba 85, Schleicher & Schuell, Dassel, Germany) on TY agar plates with a
15 relevant antibiotic, e.g., kanamycin or chloramphenicol, at 37°C for at least 21 hours. The cellulose acetate layer is located on the TY agar plate.

Each filter sandwich is specifically marked with a needle after plating, but before incubation in order to be able to
20 localize positive variants on the filter and the nitrocellulose filter with bound variants is transferred to a container with carbonate/bicarbonate buffer pH 8.5-10 and with different EDTA concentrations (0.001 mM - 100 mM). The filters are incubated at room temperature for 1 hour. The cellulose acetate filters
25 with colonies are stored on the TY-plates at room temperature until use. After incubation, residual activity is detected on plates containing 1% agarose, 0.2% starch in carbonate/bicarbonate buffer pH 8.5-10. The assay plates with nitrocellulose filters are marked the same way as the filter
30 sandwich and incubated for 2 hours. at room temperature. After removal of the filters the assay plates are stained with 10% Lugol solution. Starch degrading variants are detected as white spots on dark blue background and then identified on the storage plates. Positive variants are rescreened twice under
35 the same conditions as the first screen.

Method for obtaining the regions of interest:

There are three known 3D structures of bacterial α -

amylases. Two of *B. licheniformis* α -amylase, Brookhaven database 1BPL (Machius et al. (1995), J. Mol. Biol. 246, p. 545-559) and 1VJS (Song et al. (1996), Enzymes for Carbohydrate 163 Engineering (Prog. Biotechnol. V 12). These two structures
5 are lacking an important piece of the structure from the so-called B-domain, in the area around the two Calcium ions and one Sodium ion binding sites. We have therefore used a 3D structure of an α -amylase BA2 (WO 96/23874 which are a hybrid between BANTM (SEQ ID NO. 5) and *B. licheniformis* α -amylase (SEQ
10 ID NO. 4). On basis of the structure a model of *B. licheniformis* alpha amylase and the SP722 α -amylase has been build.

Fermentation and purification of α -amylase variants

15 Fermentation and purification may be performed by methods well known in the art.

Stability determination

20 All stability trials are made using the same set up. The method are:

The enzyme is incubated under the relevant conditions (1-4). Samples are taken at various time points, e.g., after 0, 5, 10, 15 and 30 minutes and diluted 25 times (same dilution for all taken samples) in assay buffer (0.1M 50mM Britton buffer pH
25 7.3) and the activity is measured using the Phadebas assay (Pharmacia) under standard conditions pH 7.3, 37°C.

The activity measured before incubation (0 minutes) is used as reference (100%). The decline in percent is calculated as a function of the incubation time. The table shows the residual
30 activity after, e.g., 30 minutes of incubation.

Specific activity determination

The specific activity is determined using the Phadebas assay (Pharmacia) as activity/mg enzyme. The manufactures
35 instructions are followed (see also below under "Assay for α -amylase activity).

Assays for α -Amylase Activity

1. Phadebas assay

α -amylase activity is determined by a method employing Phadebas® tablets as substrate. Phadebas tablets (Phadebas® Amylase Test, supplied by Pharmacia Diagnostic) contain a cross-linked insoluble blue-colored starch polymer which has been mixed with bovine serum albumin and a buffer substance and tabletted.

For every single measurement one tablet is suspended in a tube containing 5 ml 50 mM Britton-Robinson buffer (50 mM acetic acid, 50 mM phosphoric acid, 50 mM boric acid, 0.1 mM CaCl_2 , pH adjusted to the value of interest with NaOH). The test is performed in a water bath at the temperature of interest. The α -amylase to be tested is diluted in x ml of 50 mM Britton-Robinson buffer. 1 ml of this α -amylase solution is added to the 5 ml 50 mM Britton-Robinson buffer. The starch is hydrolyzed by the α -amylase giving soluble blue fragments. The absorbance of the resulting blue solution, measured spectrophotometrically at 620 nm, is a function of the α -amylase activity.

It is important that the measured 620 nm absorbance after 10 or 15 minutes of incubation (testing time) is in the range of 0.2 to 2.0 absorbance units at 620 nm. In this absorbance range there is linearity between activity and absorbance (Lambert-Beer law). The dilution of the enzyme must therefore be adjusted to fit this criterion. Under a specified set of conditions (temp., pH, reaction time, buffer conditions) 1 mg of a given α -amylase will hydrolyze a certain amount of substrate and a blue colour will be produced. The colour intensity is measured at 620 nm. The measured absorbance is directly proportional to the specific activity (activity/mg of pure α -amylase protein) of the α -amylase in question under the given set of conditions.

2. Alternative method

α -amylase activity is determined by a method employing the PNP-G7 substrate. PNP-G7 which is a abbreviation for p-nitrophenyl- α ,D-maltoheptaoside is a blocked oligosaccharide which can be cleaved by an endo-amylase. Following the cleavage,

the α -Glucosidase included in the kit digest the substrate to liberate a free PNP molecule which has a yellow colour and thus can be measured by visible spectrophotometry at $\lambda=405\text{nm}$. (400-420 nm.). Kits containing PNP-G7 substrate and α -Glucosidase is manufactured by Boehringer-Mannheim (cat.No. 1054635).

To prepare the substrate one bottle of substrate (BM 1442309) is added to 5 ml buffer (BM1442309). To prepare the α -Glucosidase one bottle of α -Glucosidase (BM 1462309) is added to 45 ml buffer (BM1442309). The working solution is made by mixing 5 ml α -Glucosidase solution with 0.5 ml substrate.

The assay is performed by transforming 20 μl enzyme solution to a 96 well microtitre plate and incubating at 25°C. 200 μl working solution, 25°C is added. The solution is mixed and pre-incubated 1 minute and absorption is measured every 15 sec. over 3 minutes at OD 405 nm.

The slope of the time dependent absorption-curve is directly proportional to the specific activity (activity per mg enzyme) of the α -amylase in question under the given set of conditions.

General method for random mutagenesis by use of the DOPE program

The random mutagenesis may be carried out by the following steps:

1. Select regions of interest for modification in the parent enzyme
2. Decide on mutation sites and non-mutated sites in the selected region
3. Decide on which kind of mutations should be carried out, e.g. with respect to the desired stability and/or performance of the variant to be constructed
4. Select structurally reasonable mutations.
5. Adjust the residues selected by step 3 with regard to step 4.
6. Analyze by use of a suitable dope algorithm the nucleotide distribution.
7. If necessary, adjust the wanted residues to genetic code realism (e.g., taking into account constraints resulting from

the genetic code (e.g. in order to avoid introduction of stop codons))(the skilled person will be aware that some codon combinations cannot be used in practice and will need to be adapted)

5 8. Make primers

9. Perform random mutagenesis by use of the primers

10. Select resulting α -amylase variants by screening for the desired improved properties.

Suitable dope algorithms for use in step 6 are well known in the art. One algorithm is described by Tomandl, D. et al., Journal of Computer-Aided Molecular Design, 11 (1997), pp. 29-38). Another algorithm, DOPE, is described in the following:

The dope program

15 The "DOPE" program is a computer algorithm useful to optimize the nucleotide composition of a codon triplet in such a way that it encodes an amino acid distribution which resembles most the wanted amino acid distribution. In order to assess which of the possible distributions is the most similar
20 to the wanted amino acid distribution, a scoring function is needed. In the "Dope" program the following function was found to be suited:

$$s \equiv \prod_{i=1}^N \left(\frac{x_i^{y_i} (1-x_i)^{1-y_i}}{y_i^{y_i} (1-y_i)^{1-y_i}} \right)^{w_i},$$

25

where the x_i 's are the obtained amounts of amino acids and groups of amino acids as calculated by the program, y_i 's are the wanted amounts of amino acids and groups of amino acids as defined by the user of the program (e.g. specify which of the
30 20 amino acids or stop codons are wanted to be introduced, e.g. with a certain percentage (e.g. 90% Ala, 3% Ile, 7% Val), and w_i 's are assigned weight factors as defined by the user of the program (e.g., depending on the importance of having a specific amino acid residue inserted into the position in question). N
35 is 21 plus the number of amino acid groups as defined by the

user of the program. For purposes of this function 0^0 is defined as being 1.

A Monte-Carlo algorithm (one example being the one described by Valleau, J.P. & Whittington, S.G. (1977) A guide to Mont Carlo for statistical mechanics: 1 Highways. In "Statistical Mechanics, Part A" Equilibrium Techniques ed. B.J. Berne, New York: Plenum) is used for finding the maximum value of this function. In each iteration the following steps are performed:

- 10 1. A new random nucleotide composition is chosen for each base, where the absolute difference between the current and the new composition is smaller than or equal to d for each of the four nucleotides G,A,T,C in all three positions of the codon (see below for definition of d).
- 15 2. The scores of the new composition and the current composition are compared by the use of the function s as described above. If the new score is higher or equal to the score of the current composition, the new composition is kept and the current composition is changed to the new one. If the new
- 20 score is smaller, the probability of keeping the new composition is $\exp(1000(\text{new_score} - \text{current_score}))$.

A cycle normally consists of 1000 iterations as described above in which d is decreasing linearly from 1 to 0. One hundred or more cycles are performed in an optimization

25 process. The nucleotide composition resulting in the highest score is finally presented.

EXAMPLES

30 EXAMPLE 1

Example on Homology building of Termamyl™

The overall homology of the *B. licheniformis* α -amylase (in the following referred to as Termamyl™) to other Termamyl-like α -amylases is high and the percent similarity is extremely high.

35 The similarity calculated for Termamyl™ to BSG (the *B. stearothermophilus* α -amylase having SEQ ID NO: 3), and BAN (the *B. amyloliquefaciens* α -amylase having SEQ ID NO: 5) using the

University of Wisconsin Genetics Computer Group's program GCG gave 89% and 78%, respectively. TERM has a deletion of 2 residues between residue G180 and K181 compared to BANTM and BSG. BSG has a deletion of 3 residues between G371 and I372 in comparison with BANTM and TermamylTM. Further BSG has a C-terminal extension of more than 20 residues compared to BANTM and TermamylTM. BANTM has 2 residues less and Termamyl has one residue less in the N-terminal compared to BSG.

The structure of the *B. licheniformis* (TermamylTM) and of the *B. amyloliquefaciens* α -amylase (BANTM), respectively, was model built on the structure disclosed in Appendix 1 of WO 96/23974. The structure of other Termamyl-like α -amylases (e.g. those disclosed herein) may be built analogously.

In comparison with the α -amylase used for elucidating the present structure, TermamylTM differs in that it lacks two residues around 178-182. In order to compensate for this in the model structure, the HOMOLOGY program from BIOSYM was used to substitute the residues in equivalent positions in the structure (not only structurally conserved regions) except for the deletion point. A peptide bond was established between G179(G177) and K180(K180) in TermamylTM(BANTM). The close structural relationship between the solved structure and the model structure (and thus the validity of the latter) is indicated by the presence of only very few atoms found to be too close together in the model.

To this very rough structure of TermamylTM was then added all waters (605) and ions (4 Calcium and 1 Sodium) from the solved structure (See Appendix 1 of WO 96/23874) at the same coordinates as for said solved structure using the INSIGHT program. This could be done with only few overlaps - in other words with a very nice fit. This model structure were then minimized using 200 steps of Steepest descent and 600 steps of Conjugated gradient (see Brooks et al 1983, J. Computational Chemistry 4, p.187-217). The minimized structure was then subjected to molecular dynamics, 5ps heating followed by up to 200ps equilibration but more than 35ps. The dynamics as run with the Verlet algorithm and the equilibration temperature 300K were kept using the Berendsen coupling to a water bath (Berendsen

et. al., 1984, J. Chemical Physics 81, p. 3684-3690). Rotations and translations were removed every pico second.

EXAMPLE 2

5 Method of extracting important regions for identifying α -amylase variants with improved pH stability and altered temperature activity

The X-ray structure and/or the model build structure of the enzyme of interest, here SP722 and TermamylTM, are subjected
10 to molecular dynamics simulations. The molecular dynamics simulation are made using the CHARMM (from Molecular simulations (MSI)) program or other suited program like, e.g., DISCOVER (from MSI). The molecular dynamic analysis is made in vacuum, or more preferred including crystal waters, or with the
15 enzyme embedded in water, e.g., a water sphere or a water box. The simulation are run for 300 pico seconds (ps) or more, e.g., 300-1200 ps. The isotropic fluctuations are extracted for the CA carbons of the structures and compared between the structures. Where the sequence has deletions and/or insertions
20 the isotropic fluctuations from the other structure are inserted thus giving 0 as difference in isotropic fluctuation. For explanation of isotropic fluctuations see the CHARMM manual (obtainable from MSI).

The molecular dynamics simulation can be done using
25 standard charges on the chargeable amino acids. This is Asp and Glu are negatively charged and Lys and Arg are positively charged. This condition resembles the medium pH of approximately 7. To analyze a higher or lower pH, titration of the molecule can be done to obtain the altered pKa's of the
30 standard titrateable residues normally within pH 2-10; Lys, Arg, Asp, Glu, Tyr and His. Also Ser, Thr and Cys are titrateable but are not taking into account here. Here the altered charges due to the pH has been described as both Asp and Glu are negative at high pH, and both Arg and Lys are
35 uncharged. This imitates a pH around 10 to 11 where the titration of Lys and Arg starts, as the normal pKa of these residues are around 9-11.

1. The approach used for extracting important regions for identifying α -amylase variants with high pH stability:

The important regions for constructing variants with improved pH stability are the regions which at the extreme pH display the highest mobility, i.e., regions having the highest isotropic fluctuations.

Such regions are identified by carrying out two molecular dynamics simulations: i) a high pH run at which the basic amino acids, Lys and Arg, are seen as neutral (i.e. not protonated) and the acidic amino acids, Asp and Glu, have the charge (-1) and ii) a neutral pH run with the basic amino acids, Lys and Arg, having the net charge of (+1) and the acidic amino acids having a charge of (-1).

The two run are compared and regions displaying the relatively higher mobility at high pH compared to neutral pH analysis were identified.

Introduction of residues improving general stability, e.g., hydrogen bonding, making the region more rigid (by mutations such as Proline substitutions or replacement of Glycine residues), or improving the charges or their interaction, improves the high pH stability of the enzyme.

2. The approach used for extracting regions for identifying α -amylase variants with increased activity at medium temperatures:

The important regions for constructing variants with increased activity at medium temperature was found as the difference between the isotropic fluctuations in SP722 and Termamyl, i.e., SP722 minus Termamyl CA isotrophic fluctuations, The regions with the highest mobility in the isotrophic fluctuations were selected. These regions and there residues were expected to increase the activity at medium temperatures. The activity of an alpha-amylase is only expressed if the correct mobility of certain residues are present. If the mobility of the residues is too low the activity is decreased or abandoned.

EXAMPLE 3

Construction, by localized random, doped mutagenesis, of Termamyl-like α -amylase variants having an improved Ca^{2+} stability at medium temperatures compared to the parent enzyme

5 To improve the stability at low calcium concentration of α -amylases random mutagenesis in pre-selected region was performed.

Region: Residue:
SAI: R181-W189

10 The DOPE software (see Materials and Methods) was used to determine spiked codons for each suggested change in the SAI region minimizing the amount of stop codons (see table 1). The exact distribution of nucleotides was calculated in the three positions of the codon to give the suggested population of
15 amino acid changes. The doped regions were doped specifically in the indicated positions to have a high chance of getting the desired residues, but still allow other possibilities.

Table 1:

20 Distribution of amino acid residues for each position
R181: 72% R, 2% N, 7% Q, 4% H, 4%K, 11%S
G182: 73% G, 13% A, 12% S, 2% T
K185: 95% K, 5% R
A186: 50% A, 4% N, 6% D, 1%E, 1% G, 1% K, 5% S, 31% T
25 W187: 100% W
D188: 100% D
W189: 92% W, 8% S

30 The resulting doped oligonucleotide strand is shown in table 2 as sense strand: with the wild type nucleotide and amino acid sequences and the distribution of nucleotides for each doped position.

Table 2:

35	Position	181	182	185	186	187	188	189
	Amino acid seq.	Arg	Gly	Lys	Ala	Thr	Asp	Thr
	Wt nuc. seq.	cga	ggt	aaa	gct	tgg	gat	tgg

40 Forward primer (SEQ ID NO: 15):

FSA: 5'-caa aat cgt atc tac aaa ttc 123 456 a7g 8910 tgg
gat tllg gaa gta gat tcg gaa aat-3'

Distribution of nucleotides for each doped Position

45 1: 35% A, 65% C
2: 83% G, 17% A

3: 63% G, 37% T
 4: 86% G, 14% A
 5: 85% G, 15% C
 6: 50% T, 50% C
 7: 95% A, 5% G
 8: 58% G, 37% A, 5% T
 9: 86% C, 13% A, 1% G
 10: 83% T, 17% G
 11: 92% G, 8% C

Reverse primer (SEQ ID NO: 16):
 RSA: 5'-gaa ttt gta gat acg att ttg-3'

Random mutagenesis

The spiked oligonucleotides apparent from Table 2 (which by a common term is designated FSA) and reverse primers RSA for the SA1 region and specific SEQ ID NO: 2: SP722 primers covering the SacII and the DraIII sites are used to generate PCR-library-fragments by the overlap extension method (Horton et al., Gene, 77 (1989), pp. 61-68) with an overlap of 21 base pairs. Plasmid pJE1 is template for the Polymerase Chain Reaction. The PCR fragments are cloned in the *E. coli/Bacillus* shuttle vector pDork101 (see Materials and Methods) enabling mutagenesis in *E. coli* and immediate expression in *Bacillus subtilis* preventing lethal accumulation of amylases in *E. coli*. After establishing the cloned PCR fragments in *E. coli*, a modified pUC19 fragment is digested out of the plasmid and the promoter and the mutated Termamyl gene is physically connected and expression can take place in *Bacillus*.

Screening

The library may be screened in the low calcium filter assays described in the "Material and Methods" section above.

EXAMPLE 4

Construction of variants of amylase SEQ ID NO: 1 (SP690)

The gene encoding the amylase from SEQ ID NO: 1 is located in a plasmid pTVB106 described in WO96/23873. The amylase is expressed from the amyL promoter in this construct in *Bacillus subtilis*.

A variant of the protein is delta(T183-G184)+Y243F+Q391E+K444Q. Construction of this variant is described

in WO96/23873.

Construction of delta(T183-G184) + N195F by the mega-primer method as described by Sarkar and Sommer, (1990), BioTechniques 8: 404-407.

5 Gene specific primer B1 (SEQ ID NO: 17) and mutagenic primer 101458 (SEQ ID NO: 19) were used to amplify by PCR an approximately 645 bp DNA fragment from a pTVB106-like plasmid (with the delta(T183-G184) mutations in the gene encoding the amylase from SEQ ID NO: 1).

10 The 645 bp fragment was purified from an agarose gel and used as a mega-primer together with primer Y2 (SEQ ID NO: 18) in a second PCR carried out on the same template.

The resulting approximately 1080 bp fragment was digested with restriction enzymes BstEII and AflIII and the resulting
15 approximately 510 bp DNA fragment was purified and ligated with the pTVB106-like plasmid (with the delta(T183-G184) mutations in the gene encoding the amylase from SEQ ID NO: 1) digested with the same enzymes. Competent *Bacillus subtilis* SHA273 (amylase and protease low) cells were transformed with the
20 ligation and Chloramphenicol resistant transformants and was checked by DNA sequencing to verify the presence of the correct mutations on the plasmid.

primer B1: (SEQ ID NO: 17)

5' CGA TTG CTG ACG CTG TTA TTT GCG 3'

25 primer Y2: (SEQ ID NO: 18)

5' CTT GTT CCC TTG TCA GAA CCA ATG 3'

primer 101458 (SEQ ID NO: 19):

5' GT CAT AGT TGC CGA AAT CTG TAT CGA CTT C 3'

The construction of variant: delta(T183-G184) + K185R+A186T
30 was carried out in a similar way except that mutagenic primer 101638 was used.

primer 101638: (SEQ ID NO: 20)

5' CC CAG TCC CAC GTA CGT CCC CTG AAT TTA TAT ATT TTG 3'

35 Variants: delta(T183-G184) +A186T, delta(T183-G184) +A186I, delta(T183-G184) +A186S, delta(T183-G184) +A186N are constructed by a similar method except that pTVB106-like plasmid (carrying variant delta(T183-G184) + K185R+A186T) is used as template and as the vector for the cloning purpose. The

mutagenic oligonucleotide (Oligo 1) is:

5' CC CAG TCC CAG NTCTTT CCC CTG AAT TTA TAT ATT TTG 3' (SEQ ID NO: 21)

N represents a mixture of the four bases: A, C, G, and T used in the synthesis of the mutagenic oligonucleotide. Sequencing of transformants identifies the correct codon for amino acid position 186 in the mature amylase.

Variant: delta(T183-G184) + K185R+A186T+N195F is constructed as follows:

10 PCR is carried out with primer x2 (SEQ ID NO: 22) and primer 101458 (SEQ ID NO: 19) on pTVB106-like plasmid (with mutations delta(T183-G184) + K185R+A186T). The resulting DNA fragment is used as a mega-primer together with primer Y2 (SEQ ID NO: 18) in a PCR on pTVB106-like plasmid (with mutations delta(T183-G184) + N195). The product of the second PCR is digested with restriction endonucleases Acc65I and AflIII and cloned into pTVB106 like plasmid (delta(T183-G184)+N195F) digested with the same enzymes.

primer x2: (SEQ ID NO: 22)

20 5' GCG TGG ACA AAG TTT GAT TTT CCT G 3'

Variant: delta(T183-G184) + K185R+A186T+N195F+Y243F+Q391E+K444Q is constructed as follows:

PCR is carried out with primer x2 and primer 101458 on pTVB106-like plasmid (with mutations delta(T183-G184) + K185R+A186T). The resulting DNA fragment is used as a mega-primer together with primer Y2 in a PCR on pTVB106 like plasmid (with mutations delta(T183-G184) +Y243F+Q391E+K444Q). The product of the second PCR is digested with restriction endonucleases Acc65I and AflIII and cloned into pTVB106 like plasmid (delta(T183-G184) +Y243F+Q391E+K444Q) digested with the same enzymes.

Example 5

Construction of site-directed α -amylase variants in the parent

35 SP722 α -amylase (SEQ ID NO: 2)

Construction of variants of amylase SEQ ID NO: 2 (SP722) is carried out as described below.

The gene encoding the amylase from SEQ ID NO: 2 is located

in a plasmid pTVB112 described in WO 96/23873. The amylase is expressed from the amyL promoter in this construct in *Bacillus subtilis*.

Construction of delta(D183-G184) + V56I by the mega-primer method as described by Sarkar and Sommer, 1990 (BioTechniques 8: 404-407).

Gene specific primer DA03 and mutagenic primer DA07 are used to amplify by PCR an approximately 820 bp DNA fragment from a pTVB112-like plasmid (with the delta(D183-G184) mutations in the gene encoding the α -amylase shown in SEQ ID NO: 2).

The 820 bp fragment is purified from an agarose gel and used as a mega-primer together with primer DA01 in a second PCR carried out on the same template.

The resulting approximately 920 bp fragment is digested with restriction enzymes NgoM I and Aat II and the resulting approximately 170 bp DNA fragment is purified and ligated with the pTVB112-like plasmid (with the delta(D183-G184) mutations in the gene encoding the amylase shown in SEQ ID NO: 2) digested with the same enzymes. Competent *Bacillus subtilis* SHA273 (amylase and protease low) cells are transformed with the ligation and Chloramphenicol resistant transformants are checked by DNA sequencing to verify the presence of the correct mutations on the plasmid.

primer DA01: (SEQ ID NO: 23)

5' CCTAATGATGGGAATCACTGG 3'

primer DA03: (SEQ ID NO:24)

5' GCATTGGATGCTTTTGAACAACCG 3'

primer DA07 (SEQ ID NO:25):

5' CGCAAATGATATCGGGTATGGAGCC 3'

Variants: delta(D183-G184) + K108L, delta(D183-G184) + K108Q, delta(D183-G184) + K108E, delta(D183-G184) + K108V, were constructed by the mega-primer method as described by Sarkar and Sommer, 1990 (BioTechniques 8: 404-407):

PCR is carried out with primer DA03 and mutagenesis primer DA20 on pTVB112-like plasmid (with mutations delta(D183-G184)). The resulting DNA fragment is used as a mega-primer together with primer DA01 in a PCR on pTVB112-like plasmid (with

mutations delta(D183-G184)). The approximately 920 bp product of the second PCR is digested with restriction endonucleases Aat II and Mlu I and cloned into pTVB112-like plasmid (delta(D183-G184)) digested with the same enzymes.

5 primer DA20 (SQ ID NO:26):

5' GTGATGAACCACSWAGGTGGAGCTGATGC 3'

S represents a mixture of the two bases: C and G used in the synthesis of the mutagenic oligonucleotide and W represents a mixture of the two bases: A and T used in the synthesis of
10 the mutagenic oligonucleotide.

Sequencing of transformants identifies the correct codon for amino acid position 108 in the mature amylase.

Construction of the variants: delta(D183-G184) + D168A, delta(D183-G184) + D168I, delta(D183-G184) + D168V, delta(D183-
15 G184) + D168T is carried out in a similar way except that mutagenic primer DA14 is used.

primer DA14 (SEQ ID NO:27):

5' GATGGTGTATGGRYCAATCACGACAATTCC 3'

R represents a mixture of the two bases: A and G used in
20 the synthesis of the mutagenic oligonucleotide and Y represents a mixture of the two bases: C and T used in the synthesis of the mutagenic oligonucleotide.

Sequencing of transformants identifies the correct codon for amino acid position 168 in the mature amylase.

25 Construction of the variant: delta(D183-G184) + Q169N is carried out in a similar way except that mutagenic primer DA15 is used.

primer DA15 (SEQ ID NO:28):

5' GGTGTATGGGATAACTCACGACAATTCC 3'

30 Construction of the variant: delta(D183-G184) + Q169L is carried out in a similar way except that mutagenic primer DA16 is used.

primer DA16 (SEQ ID NO:29):

5' GGTGTATGGGATCTCTCACGACAATTCC 3'

35 Construction of the variant: delta(D183-G184) + Q172N is carried out in a similar way except that mutagenic primer DA17 is used.

primer DA17 (SEQ ID NO:30):

5' GGGATCAATCACGAAATTTCCAAAATCGTATC 3'

Construction of the variant: delta(D183-G184) + Q172L is carried out in a similar way except that mutagenic primer DA18 is used.

5 primer DA18 (SEQ ID NO:31):

5' GGGATCAATCACGACTCTTCCAAAATCGTATC 3'

Construction of the variant: delta(D183-G184) + L201I is carried out in a similar way except that mutagenic primer DA06 is used.

10 primer DA06 (SEQ ID NO:32):

5' GGAAATTATGATTATATCATGTATGCAGATGTAG 3'

Construction of the variant: delta(D183-G184) + K269S is carried out in a similar way except that mutagenic primer DA09 is used.

15 primer DA09 (SEQ ID NO:33):

5' GCTGAATTTTGGTCGAATGATTTAGGTGCC 3'

Construction of the variant: delta(D183-G184) + K269Q is carried out in a similar way except that mutagenic primer DA11 is used.

20 primer DA11 (SEQ ID NO:34):

5' GCTGAATTTTGGTCGAATGATTTAGGTGCC 3'

Construction of the variant: delta(D183-G184) + N270Y is carried out in a similar way except that mutagenic primer DA21 is used.

25 primer DA21 (SEQ ID NO:35):

5' GAATTTTGAAGTACGATTTAGGTCCG 3'

Construction of the variants: delta(D183-G184) + L272A, delta(D183-G184) + L272I, delta(D183-G184) + L272V, delta(D183-G184) + L272T is carried out in a similar way except that

30 mutagenic primer DA12 is used.

primer DA12 (SEQ ID NO:36):

5' GGAAAACGATRYCGGTGCCTTGGAGAAC 3'

R represents a mixture of the two bases: A and G used in the synthesis of the mutagenic oligonucleotide and Y represents a mixture of the two bases: C and T used in the synthesis of the

35 mutagenic oligonucleotide.

Sequencing of transformants identifies the correct codon for amino acid position 272 in the mature amylase.

Construction of the variants: delta(D183-G184) + L275A, delta(D183-G184) + L275I, delta(D183-G184) + L275V, delta(D183-G184) + L275T is carried out in a similar way except that mutagenic primer DA13 is used.

5 primer DA13 (SEQ ID NO:37):

5' GATTTAGGTGCCTRYCAGAACTATTTA 3'

R represents a mixture of the two bases: A and G used in the synthesis of the mutagenic oligonucleotide and Y represents a mixture of the two bases: C and T used in the synthesis of the
10 mutagenic oligonucleotide.

Sequencing of transformants identifies the correct codon for amino acid position 275 in the mature amylase.

Construction of the variant: delta(D183-G184) + Y295E is carried out in a similar way except that mutagenic primer DA08
15 is used.

primer DA08 (SEQ ID NO:38):

5' CCCCCTTCATGAGAATCTTTATAACG 3'

Construction of delta(D183-G184) + K446Q by the mega-primer method as described by Sarkar and Sommer, 1990 (BioTechniques 8:
20 404-407):

Gene specific primer DA04, annealing 214-231 bp downstream relative to the STOP-codon and mutagenic primer DA10 were used to amplify by PCR an approximately 350 bp DNA fragment from a pTVB112-like plasmid (with the delta(D183-G184) mutations in
25 the gene encoding the amylase depicted in SEQ ID NO: 2).

The resulting DNA fragment is used as a mega-primer together with primer DA05 in a PCR on pTVB112 like plasmid (with mutations delta(D183-G184)). The app. 460 bp product of the second PCR is digested with restriction endonucleases SnaB
30 I and Not I and cloned into pTVB112 like plasmid (delta(D183-G184)) digested with the same enzymes.

primer DA04 (SEQ ID NO:39):

5' GAATCCGAACCTCATTACACATTCG 3'

primer DA05 (SEQ ID NO:40):

35 5' CGGATGGACTCGAGAAGGAAATACCACG 3'

primer DA10 (SEQ ID NO:41):

5' CGTAGGGCAAATCAGGCCGGTCAAGTTTGG 3'

Construction of the variants: delta(D183-G184) + K458R is

carried out in a similar way except that mutagenic primer DA22 is used.

primer DA22 (SEQ ID NO:42):

5' CATAACTGGAAATCGCCCGGGAACAGTTACG 3'

- 5 Construction of the variants: delta(D183-G184) + P459S and delta(D183-G184) + P459T is carried out in a similar way except that mutagenic primer DA19 is used.

primer DA19 (SEQ ID NO:43):

5' CTGGAAATAAAWCCGGAACAGTTACG 3'

- 10 W represents a mixture of the two bases: A and T used in the synthesis of the mutagenic oligonucleotide.

Sequencing of transformants identifies the correct codon for amino acid position 459 in the mature amylase.

- Construction of the variants: delta(D183-G184) + T461P is carried out in a similar way except that mutagenic primer DA23 is used.

primer DA23 (SEQ ID NO:44):

5' GGAAATAAACCAGGACCCGTTACGATCAATGC 3'

- Construction of the variant: delta(D183-G184) + K142R is carried out in a similar way except that mutagenic primer DA32 is used.

Primer DA32 (SEQ ID NO: 45):

5' GAGGCTTGGACTIONAGGTTTGATTTTCCAG 3'

- Construction of the variant: delta(D183-G184) + K269R is carried out in a similar way except that mutagenic primer DA31 is used.

Primer DA31 (SEQ ID NO: 46):

5' GCTGAATTTTGGCGCAATGATTTAGGTGCC 3'

30 **Example 6**

Construction of site-directed α -amylase variants in the parent Termamyl α -amylase (SEQ ID NO: 4)

- The amyL gene, encoding the Termamyl α -amylase is located in plasmid pDN1528 described in WO 95/10603 (Novo Nordisk).
35 Variants with substitutions N265R and N265D, respectively, of said parent α -amylase are constructed by methods described in WO 97/41213 or by the "megaprimer" approach described above.

Mutagenic oligonucleotides are:

Primer bl1 for the N265R substitution:

5' PCC AGC GCG CCT AGG TCA CGC TGC CAA TAT TCA G (SEQ ID NO:
5 56)

Primer bl2 for the N265D substitution:

5' PCC AGC GCG CCT AGG TCA TCC TGC CAA TAT TCA G (SEQ ID NO:
57)

P represents a phosphate group.

10

Example 7

Determination of pH stability at alkaline pH of variants of the
parent α -Amylase having the amino acid sequence shown in SEQ ID
NO:2.

15 In this serie of analysis purified enzyme samples were used.
The measurements were made using solutions of the respective
variants in 100 mM CAPS buffer adjusted to pH 10.5. The
solutions were incubated at 75°C.

20 After incubation for 20 and 30 min the residual activity was
measured using the PNP-G7 assay (described in the "Materials
and Methods" section above). The residual activity in the
samples was measured using Britton Robinson buffer pH 7.3. The
decline in residual activity was measured relative to a
corresponding reference solution of the same enzyme at 0
25 minutes, which has not been incubated at high pH and 75°C.

The percentage of the initial activity as a function is shown
in the table below for the parent enzyme (SEQ ID NO: 2) and for
the variants in question.

Variant	Residual activity after 20 min	Residual activity after 30 min
Δ (D183-G184)+M323L	56 %	44 %
Δ (D183-G184)+M323L+R181S	67 %	55 %
Δ (D183-G184)+M323L+A186T	62 %	50 %

30 In an other series of analysis culture supernatants were
used. The measurements were made using solutions of the
respective variants in 100 mM CAPS buffer adjusted to pH 10.5.

The solutions were incubated at 80°C.

After incubation for 30 minutes the residual activity was measured using the Phadebas assay (described in the "Materials and Method" section above. The residual activity in the samples
5 was measured using Britton Robinson buffer pH 7.3. The decline in residual activity was measured relative to a corresponding reference solution of the same enzyme at 0 minutes, which has not been incubated at high pH and 80°C.

The percentage of the initial activity as a function is shown
10 in the table below for the parent enzyme (SEQ ID NO: 2) and for the variants in question.

Variant	Residual activity after 30 min
Δ (D183-G184)	4 %
Δ (D183-G184)+P459T	25 %
Δ (D183-G184)+K458R	31 %
Δ (D183-G184)+K311R	10 %

Example 8

Determination of calcium stability at alkaline pH of variants
15 of the parent α -Amylase having the amino acid sequence shown in
SEQ ID NO: 1, SEQ ID NO: 2 and SEQ ID NO: 4.

A: Calcium stability of variants of the sequence in SEQ ID NO:1

The measurement were made using solutions of the respective
20 variants in 100 mM CAPS buffer adjusted to pH 10.5 to which polyphosphate was added (at time t=0) to give a final concentration of 2400 ppm. The solutions were incubated at 50°C.

After incubation for 20 and 30 minutes the residual activity was measured using the PNP-G7 assay (described above). The
25 residual activity in the samples was measured using Britton Robinson buffer pH 7.3. The decline in residual activity was measured relative to a corresponding reference solution of the same enzyme at 0 minutes, which has not been incubated at high pH and 50°C.

30 The percentage of the initial activity as a function is shown in the table below for the parent enzyme (SEQ ID NO: 1) and for

the variants in question.

Variant	Residual activity after 20 min	Residual activity after 30 min
Δ (T183-G184)	32 %	19 %
Δ (T183-G184)+ A186T	36 %	23 %
Δ (T183-G184)+K185R+A186T	45 %	29 %
Δ (T183-G184)+A186I	35 %	20 %
Δ (T183-G184)+N195F	44 %	n.d.

n.d.= Not determinated

B: Calcium stability of variants of the sequence in SEQ ID NO:2

- 5 In this series of analysis purified samples of enzymes were used. The measurement were made using solutions of the respective variants in 100 mM CAPS buffer adjusted to pH 10.5 to which polyphosphate was added (at time t=0) to give a final concentration of 2400 ppm. The solutions were incubated at 50°C.
- 10 After incubation for 20 and 30 minutes the residual activity was measured using the PNP-G7 assay (described above). The residual activity in the samples was measured using Britton Robinson buffer pH 7.3. The decline in residual activity was measured relative to a corresponding reference solution of the
- 15 same enzyme at 0 minutes, which has not been incubated at high pH and 50°C.

The percentage of the initial activity as a function is shown in the table below for the parent enzyme (SEQ ID NO: 2) and for the variants in question.

Variant	Residual activity after 20 min	Residual activity after 30 min
Δ (D183-G184)+M323L	21 %	13 %
Δ (D183-G184)+M323L+R181S	32 %	19 %
Δ (D183-G184)+M323L+A186T	28 %	17 %
Δ (D183-G184)+M323L+A186R	30 %	18 %

20

Variant	Residual activity after 20 min	Residual activity after 30 min
---------	-----------------------------------	-----------------------------------

Δ (D183-G184)	30%	20%
Δ (D183-G184)+N195F	55%	44%

In this serie of analysis culture supernatants were used. The measurement were made using solutions of the respective variants in 100 mM CAPS buffer adjusted to pH 10.5 to which
5 polyphosphate was added (at time t=0) to give a final concentration of 2400 ppm. The solutions were incubated at 50°C.

After incubation for 30 minutes the residual activity was measured using the Phadebas assay as described above. The residual activity in the samples was measured using Britton
10 Robinson buffer pH 7.3. The decline in residual activity was measured relative to a corresponding reference solution of the same enzyme at 0 minutes, which has not been incubated at high pH and 50°C.

The percentage of the initial activity as a function is shown
15 in the table below for the parent enzyme (SEQ ID NO: 2) and for the variants in question.

Variant	Residual activity after 30 min
Δ (D183-G184)	0 %
Δ (D183-G184)+P459T	19 %
Δ (D183-G184)+K458R	18 %
Δ (D183-G184)+T461P	13 %
Δ (D183-G184)+E346Q+K385R	4 %

C: Calcium stability of variants of the sequence in SEQ ID NO:4

20 The measurement were made using solutions of the respective variants in 100 mM CAPS buffer adjusted to pH 10.5 to which polyphosphate was added (at time t=0) to give a final concentration of 2400 ppm. The solutions were incubated at 60°C for 20 minutes.

25 After incubation for 20 minutes the residual activity was measured using the PNP-G7 assay (described above). The residual activity in the samples was measured using Britton Robinson buffer pH 7.3. The decline in residual activity was measured

relative to a corresponding reference solution of the same enzyme at 0 minutes, which has not been incubated at high pH and 60°C.

The percentage of the initial activity as a function is shown in the table below for the parent enzyme (SEQ ID NO: 4) and for the variants in question.

Variant	Residual activity after 20 min
Termamyl (SEQ ID NO: 4)	17 %
N265R	28 %
N265D	25 %

Example 9:

10 Activity measurement at medium temperature of α -Amylases having the amino acid sequence shown in SEQ ID NO: 1.

A: α -Amylase activity of variants of the sequence in SEQ ID NO: 1

15 The measurement were made using solutions of the respective variants in 50 mM Britton Robinson buffer adjusted to pH 7.3 and using the Phadebas assay described above. The activity in the samples was measured at 37°C using 50 mM Britton Robinson buffer pH 7.3 and at 25°C using 50 mM CAPS buffer pH 10.5.

20 The temperature dependent activity and the percentage of the activity at 25°C relative to the activity at 37°C are shown in the table below for the parent enzyme (SEQ ID NO: 1) and for the variants in question.

Variant	NU/mg 25°C	NU/mg 37°C	NU (25°C) / NU (37°C)
SP690	1440	35000	4.1 %
Δ (T183-G184)	2900	40000	7.3 %
Δ (T183-G184)+K269S	1860	12000	15.5 %
Δ (Q174)	3830	38000	7.9 %

Another measurement was made using solutions of the

respective variants in 50 mM Britton Robinson buffer adjusted to pH 7.3 and using the Phadebas assay described above. The activity in the samples was measured at 37°C and 50°C using 50 mM Britton Robinson buffer pH 7.3.

- 5 The temperature dependent activity and the percentage of the activity at 37°C relative to the activity at 50°C is shown in the table below for the parent enzyme (SEQ ID NO: 1) and for the variants in question.

Variant	NU/mg 37°C	NU/mg 50°C	NU (37°C) / NU (50°C)
SP690 (seq ID NO: 1)	13090	21669	60 %
K269Q	7804	10063	78 %

10

B: α -Amylase activity of variants of the sequence in SEQ ID NO:2

- 15 The measurement were made using solutions of the respective variants in 50 mM Britton Robinson buffer adjusted to pH 7.3 and using the Phadebas assay described above. The activity in the samples was measured at both 25°C and 37°C using 50 mM Britton Robinson buffer pH 7.3.

- 20 The temperature dependent activity and the percentage of the activity at 25°C relative to the activity at 37°C is shown in the table below for the parent enzyme (SEQ ID NO: 2) and for the variants in question.

Variant	NU/mg 25°C	NU/mg 37°C	NU (25°C) / NU (37°C)
Δ (D183-G184)+M323L	3049	10202	30 %
Δ (D183-G184)+M323L+R181S	18695	36436	51 %

C: α -Amylase activity of variants of the sequence in SEQ ID

NO:4

- 25 The measurement were made using solutions of the respective variants in 50 mM Britton Robinson buffer adjusted to pH 7.3 and using the Phadebas assay described above. The activity in

the samples was measured at both 37°C using 50 mM Britton Robinson buffer pH 7.3 and at 60°C using 50 mM CAPS buffer pH 10.5.

The temperature dependent activity and the percentage of the activity at 37°C relative to the activity at 60°C is shown in the table below for the parent enzyme (SEQ ID NO: 4) and for the variants in question.

Variant	NU/mg 37°C	NU/mg 60°C	NU(37°C) / NU(60°C)
Termamyl	7400	4350	170 %
Q264S	10000	4650	215 %

Example 10Construction of variants of parent hybrid BAN:1-300/Termamyl:301-483 α -amylase

5 Plasmid pTVB191 contains the gene encoding hybrid α -amylase BAN:1-300/Termamyl:301-483 as well as an origin of replication functional in *Bacillus subtilis* and the *cat* gene conferring chloramphenicol resistance.

10 Variant BM4 (F290E) was constructed using the megaprimer approach (Sarkar and Sommer, 1990) with plasmid pTVB191 as template.

Primer p1 (SEQ ID NO: 52) and mutagenic oligonucleotide bm4 (SEQ ID NO: 47) were used to amplify a 444 bp fragment with polymerase chain reaction (PCR) under standard conditions.

15 This fragment was purified from an agarose gel and used as 'Megaprimer' in a second PCR with primer p2 (SEQ ID NO: 53) resulting in a 531 bp fragment. This fragment was digested with restriction endonucleases HindIII and Tth111I. The 389 bp fragment produced by this was ligated into plasmid pTVB191 that
20 had been cleaved with the same two enzymes. The resulting plasmid was transformed into *B. subtilis* SHA273. Chloramphenicol resistant clones were selected by growing the transformants on plates containing chloramphenicol as well as insoluble starch. Clones expressing an active α -amylase were isolated by selecting
25 clones that formed halos after staining the plates with iodine vapour. The identity of the introduced mutations was confirmed by DNA sequencing.

30 Variants BM5(F290K), BM6(F290A), BM8(Q360E) and BM11(N102D) were constructed in a similar way. Details of their construction are given below.

Variant: BM5(F290K)

mutagenic oligonucleotide: bm5 (SEQ ID NO: 48)

Primer (1st PCR): p1 (SEQ ID NO: 52)

35 Size of resulting fragment: 444 bp

Primer (2nd PCR): p2 (SEQ ID NO: 53)

Restriction endonucleases: HindIII, Tth111I

Size of cleaved fragment: 389 bp

Variant: BM6(F290A)

mutagenic oligonucleotide: bm6 (SEQ ID NO: 49)

Primer (1st PCR): p1 (SEQ ID NO: 52)

5 Size of resulting fragment: 444 bp

Primer (2nd PCR): p2 (SEQ ID NO: 53)

Restriction endonucleases: HindIII, Tth111I

Size of cleaved fragment: 389 bp

10 Variant: BM8(Q360E)

mutagenic oligonucleotide: bm8 (SEQ ID NO: 50)

Primer (1st PCR): p1 (SEQ ID NO: 52)

Size of resulting fragment: 230 bp

Primer (2nd PCR): p2 (SEQ ID NO: 53)

15 Restriction endonucleases: HindIII, Tth111I

Size of cleaved fragment: 389 bp

Variant: BM11(N102D)

mutagenic oligonucleotide: bm11 (SEQ ID NO: 51)

20 Primer (1st PCR): p3 (SEQ ID NO: 54)

Size of resulting fragment: 577

Primer (2nd PCR): p4 (SEQ ID NO: 55)

Restriction endonucleases: HindIII, PvuI

Size of cleaved fragment: 576

25

Mutagenic oligonucleotides:

bm4 (SEQ ID NO: 47): F290E

primer 5' GTG TTT GAC GTC CCG CTT CAT GAG AAT TTA CAG G

bm5 (SEQ ID NO: 48): F290K

30 primer 5' GTG TTT GAC GTC CCG CTT CAT AAG AAT TTA CAG G

bm6 (SEQ ID NO: 49): F290A

primer 5' GTG TTT GAC GTC CCG CTT CAT GCC AAT TTA CAG G

bm8 (SEQ ID NO: 50): Q360E

primer 5' AGG GAA TCC GGA TAC CCT GAG GTT TTC TAC GG

35 bm11 (SEQ ID NO: 51): N102D

primer 5' GAT GTG GTT TTG GAT CAT AAG GCC GGC GCT GAT G

Other primers:

p1: 5' CTG TTA TTA ATG CCG CCA AAC C (SEQ ID NO: 52)
p2: 5' G GAA AAG AAA TGT TTA CGG TTG CG (SEQ ID NO: 53)
p3: 5' G AAA TGA AGC GGA ACA TCA AAC ACG (SEQ ID NO: 54)
p4: 5' GTA TGA TTT AGG AGA ATT CC (SEQ ID NO: 55)

5

Example 11

α -Amylase activity at alkaline pH of variants of parent BAN:1-300/Termamyl:301-483 hybrid α -amylase.

10 The measurements were made using solutions for the respective enzymes and utilizing the Phadebas assay (described above). The activity was measured after incubating for 15 minutes at 30°C in 50 mM Britton-Robinson buffer adjusted to the indicated pH by NaOH.

15 NU/mg enzyme

pH	wt	Q360E	F290A	F290K	F290E	N102D
8.0	5300	7800	8300	4200	6600	6200
9.0	1600	2700	3400	2100	1900	1900

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CLAIMS

1. A variant of a parent Termamyl-like α -amylase, which variant has α -amylase activity, said variant comprises one or more mutations corresponding to the following mutations in the amino acid sequence shown in SEQ ID NO: 2:

T141, K142, F143, D144, F145, P146, G147, R148, G149,
Q174, R181, G182, D183, G184, K185, A186, W189, S193, N195
H107, K108, G109, D166, W167, D168, Q169, S170, R171, Q172, F173,
10 F267, W268, K269, N270, D271, L272, G273, A274, L275, K311,
E346, K385, G456, N457, K458, P459, G460, T461, V462, T463.

2. The variant according to claim 1, which variant has one or more of the following substitutions or deletions:

15 T141A, D, R, N, C, E, Q, G, H, I, L, K, M, F, P, S, W, Y, V;
K142A, D, R, N, C, E, Q, G, H, I, L, M, F, P, S, T, W, Y, V;
F143A, D, R, N, C, E, Q, G, H, I, L, K, M, P, S, T, W, Y, V;
D144A, R, N, C, E, Q, G, H, I, L, K, M, F, P, S, T, W, Y, V;
F145A, D, R, N, C, E, Q, G, H, I, L, K, M, P, S, T, W, Y, V;
20 P146A, D, R, N, C, E, Q, G, H, I, L, K, M, F, S, T, W, Y, V;
G147A, D, R, N, C, E, Q, H, I, L, K, M, F, P, S, T, W, Y, V;
R148A, D, N, C, E, Q, G, H, I, L, K, M, F, P, S, T, W, Y, V;
G149A, D, R, N, C, E, Q, H, I, L, K, M, F, P, S, T, W, Y, V;
R181*, A, D, N, C, E, Q, G, H, I, L, K, M, F, P, S, T, W, Y, V;
25 G182*, A, D, R, N, C, E, Q, H, I, L, K, M, F, P, S, T, W, Y, V;
D183*, A, R, N, C, E, Q, G, H, I, L, K, M, F, P, S, T, W, Y, V;
G184*, A, R, D, N, C, E, Q, H, I, L, K, M, F, P, S, T, W, Y, V;
K185A, D, R, N, C, E, Q, G, H, I, L, M, F, P, S, T, W, Y, V;
A186D, R, N, C, E, Q, G, H, I, L, K, M, F, P, S, T, W, Y, V;
30 W189A, D, R, N, C, E, Q, G, H, I, L, K, M, F, P, S, T, Y, V;
S193A, D, R, N, C, E, Q, G, H, I, L, K, M, F, P, T, W, Y, V;
N195A, D, R, C, E, Q, G, H, I, L, K, M, F, P, S, T, W, Y, V;
H107A, D, R, N, C, E, Q, G, I, L, K, M, F, P, S, T, W, Y, V;
K108A, D, R, N, C, E, Q, G, H, I, L, M, F, P, S, T, W, Y, V;
35 G109A, D, R, N, C, E, Q, H, I, L, K, M, F, P, S, T, W, Y, V;
D166A, R, N, C, E, Q, G, H, I, L, K, M, F, P, S, T, W, Y, V;
W167A, D, R, N, C, E, Q, G, H, I, L, K, M, F, P, S, T, Y, V;
D168A, R, N, C, E, Q, G, H, I, L, K, M, F, P, S, T, W, Y, V;

Q169A, D, R, N, C, E, G, H, I, L, K, M, F, P, S, T, W, Y, V;
 S170A, D, R, N, C, E, Q, G, H, I, L, K, M, F, P, T, W, Y, V;
 R171A, D, N, C, E, Q, G, H, I, L, K, M, F, P, S, T, W, Y, V;
 Q172A, D, R, N, C, E, G, H, I, L, K, M, F, P, S, T, W, Y, V;
 5 F173A, D, R, N, C, E, Q, G, H, I, L, K, M, P, S, T, W, Y, V;
 Q174*, A, D, R, N, C, E, G, H, I, L, K, M, F, P, S, T, W, Y, V;
 F267A, D, R, N, C, E, Q, G, H, I, L, K, M, P, S, T, W, Y, V;
 W268A, D, R, N, C, E, Q, G, H, I, L, K, M, F, P, S, T, Y, V;
 K269A, D, R, N, C, E, Q, G, H, I, L, M, F, P, S, T, W, Y, V;
 10 N270A, D, R, C, E, Q, G, H, I, L, K, M, F, P, S, T, W, Y, V;
 D271A, R, N, C, E, Q, G, H, I, L, K, M, F, P, S, T, W, Y, V;
 L272A, D, R, N, C, E, Q, G, H, I, K, M, F, P, S, T, W, Y, V;
 G273A, D, R, N, C, E, Q, H, I, L, K, M, F, P, S, T, W, Y, V;
 A274D, R, N, C, E, Q, G, H, I, L, K, M, F, P, S, T, W, Y, V;
 15 L275A, D, R, N, C, E, Q, G, H, I, K, M, F, P, S, T, W, Y, V;
 K311A, D, R, N, C, E, Q, G, H, I, L, M, F, P, S, T, W, Y, V;
 E346A, D, R, N, C, Q, G, H, I, K, L, M, F, P, S, T, W, Y, V;
 K385A, D, R, N, C, E, Q, G, H, I, L, M, F, P, S, T, W, Y, V;
 G456A, D, R, N, C, E, Q, H, I, L, K, M, F, P, S, T, W, Y, V;
 20 N457A, D, R, C, E, Q, G, H, I, L, K, M, F, P, S, T, W, Y, V;
 K458A, D, R, N, C, E, Q, G, H, I, L, M, F, P, S, T, W, Y, V;
 P459A, D, R, N, C, E, Q, G, H, I, L, K, M, F, S, T, W, Y, V;
 G460A, D, R, N, C, E, Q, H, I, L, K, M, F, P, S, T, W, Y, V;
 T461A, D, R, N, C, E, Q, G, H, I, L, K, M, F, P, S, W, Y, V;
 25 V462A, D, R, N, C, E, Q, G, H, I, L, K, M, F, P, S, T, W, Y;
 T463A, D, R, N, C, E, Q, G, H, I, L, K, M, F, P, S, W, Y, V.

3. The variant according to claim 2, wherein the variant has one or more of the following substitutions or deletions:

30 K142R; S193P; N195F; K269R,Q; N270Y,R,D; K311R; E346Q; K385R;
 K458R; P459T; T461P; Q174*; R181Q,N,S; G182T,S,N; D183*; G184*;
 K185A,R,D,C,E,Q,G,H,I,L,M,N,F,P,S,T,W,Y,V; A186T,S,N,I,V,R;
 W189T,S,N,Q.

35 4. The variant according to claims 1-3, wherein the variant has a deletion in position D183 + G184, and further one or more of the following substitutions or deletions: K142R; S193P; N195F; K269R,Q; N270Y,R,D; K311R; E346Q; K385R; K458R; P459T; T461P;

Q174*; R181Q,N,S; G182T,S,N; D183*; G184*;
 K185A,R,D,C,E,Q,G,H,I,L,M,N,F,P,S,T,W,Y,V; A186T,S,N,I,V,R;
 W189T,S,N,Q.

5 5. The variant according to any of claims 1-4, wherein the variant exhibits an alteration in at least one of the following properties relative to the parent α -amylase:

- i) improved pH stability at a pH from 8 to 10.5; and/or
- ii) improved Ca^{2+} stability at pH 8 to 10.5, and/or
- 10 iii) increased specific activity at temperatures from 10 to 60°C, preferably 20-50°C, especially 30-40°C.

6. The variant according to any of claims 1-5, exhibiting improved stability at pH 8 to 10.5, having mutations in one or
 15 more of the position(s) corresponding to the following positions (using SEQ ID NO: 2 numbering): T141, K142, F143, D144, F145, P146, G147, R148, G149, R181, A186, S193, N195, K269, N270, K311, K458, P459, T461.

20 7. The variant according to claim 6, which variant has one or more of the following substitutions:

- T141A,D,R,N,C,E,Q,G,H,I,L,K,M,F,P,S,W,Y,V;
- K142A,D,R,N,C,E,Q,G,H,I,L,M,F,P,S,T,W,Y,V;
- F143A,D,R,N,C,E,Q,G,H,I,L,K,M,P,S,T,W,Y,V;
- 25 D144A,R,N,C,E,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V;
- F145A,D,R,N,C,E,Q,G,H,I,L,K,M,P,S,T,W,Y,V;
- P146A,D,R,N,C,E,Q,G,H,I,L,K,M,F,S,T,W,Y,V;
- G147A,D,R,N,C,E,Q,H,I,L,K,M,F,P,S,T,W,Y,V;
- R148A,D,N,C,E,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V;
- 30 G149A,D,R,N,C,E,Q,H,I,L,K,M,F,P,S,T,W,Y,V;
- K181A,D,R,N,C,E,Q,G,H,I,L,M,F,P,S,T,W,Y,V;
- A186D,R,N,C,E,Q,G,H,I,L,P,K,M,F,S,T,W,Y,V;
- S193A,D,R,N,C,E,Q,G,H,I,L,K,M,F,P,T,W,Y,V;
- N195A,D,R,C,E,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V;
- 35 K269A,D,R,N,C,E,Q,G,H,I,L,M,F,P,S,T,W,Y,V;
- N270A,D,R,C,E,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V;
- K311A,D,R,N,C,E,Q,G,H,I,L,M,F,P,S,T,W,Y,V;

K458A, D, R, N, C, E, Q, G, H, I, L, M, F, P, S, T, W, Y, V;

P459A, D, R, N, C, E, Q, G, H, I, L, K, M, F, S, T, W, Y, V;

T461A, D, R, N, C, E, Q, G, H, I, L, K, M, F, P, S, W, Y, V.

- 5 8. The variant according to claim 7, wherein the variant has one or more of the following substitutions: K142R, R181S, A186T, S193P, N195F, K269R, N270Y, K311R, K458R, P459T and T461P.

- 10 9. The variant according to claims 1-5, exhibiting improved Ca^{2+} stability at pH 8 to 10.5, having mutations in one or more of the following positions (using the SEQ ID NO: 2 numbering): R181, G182, D183, G184, K185, A186, W189, N195, N270, E346, K385, K458, P459.

- 15 10. The variant according to claim 9, which variant has one or more of the following substitutions or deletions:

R181*, A, D, N, C, E, Q, G, H, I, L, K, M, F, P, S, T, W, Y, V;

G182*, A, D, R, N, C, E, Q, H, I, L, K, M, F, P, S, T, W, Y, V;

D183*, A, R, N, C, E, Q, G, H, I, L, K, M, F, P, S, T, W, Y, V;

- 20 G184*, A, R, D, N, C, E, Q, H, I, L, K, M, F, P, S, T, W, Y, V;

K185A, D, R, N, C, E, Q, G, H, I, L, M, F, P, S, T, W, Y, V;

A186D, R, N, C, E, Q, G, H, I, L, K, M, F, P, S, T, W, Y, V;

W189A, D, R, N, C, E, Q, G, H, I, L, K, M, F, P, S, T, Y, V;

N195A, D, R, C, E, Q, G, H, I, L, K, M, F, P, S, T, W, Y, V;

- 25 N270A, R, D, N, C, E, Q, H, I, L, K, M, F, P, S, T, W, Y, V;

E346A, R, D, N, C, Q, G, H, I, L, K, M, F, P, S, T, W, Y, V;

K385A, R, D, N, C, E, Q, G, H, I, L, M, F, P, S, T, W, Y, V;

K458A, R, D, N, C, E, Q, G, H, I, L, M, F, P, S, T, W, Y, V;

P459A, R, D, N, C, E, Q, G, H, I, L, K, M, F, S, T, W, Y, V.

30

11. The variant according to claim 10, wherein the variant has one or more of the following substitutions or deletions:

R181Q, N; G182T, S, N; D183*; G184*;

K185A, R, D, C, E, Q, G, H, I, L, M, N, F, P, S, T, W, Y, V; A186T, S, N, I, V;

- 35 W189T, S, N, Q; N195F; N270R, D; E346Q; K385R; K458R; P459T.

12. A variant according to claims 1-11, wherein the parent Termamyl-like α -amylase is selected from:

the *Bacillus* strain NCIB 12512 α -amylase having the sequence shown in SEQ ID NO: 1;

the *B. amyloliquefaciens* α -amylase having the sequence shown in SEQ ID NO: 5;

5 the *B. licheniformis* α -amylase having the sequence shown in SEQ ID NO: 4.

13. The variant according to claims 1-5, exhibiting increased specific activity at a temperatures from 10 to 60°C, preferably
10 20-50°C, especially 30-40°C, having mutation(s) in one or more of the following positions (using the SEQ ID NO: 2 numbering):
H107, K108, G109, D166, W167, D168, Q169, S170, R171, Q172,
F173, Q174, D183, G184, N195, F267, W268, K269, N270, D271, L272,
G273, A274, L275, G456, N457, K458, P459, G460, T461, V462,
15 T463.

14. The variant according to claim 13, which variant has one or more of the following substitutions:

H107A, D, R, N, C, E, Q, G, I, L, K, M, F, P, S, T, W, Y, V;
20 K108A, D, R, N, C, E, Q, G, H, I, L, M, F, P, S, T, W, Y, V;
G109A, D, R, N, C, E, Q, H, I, L, K, M, F, P, S, T, W, Y, V;
D166A, R, N, C, E, Q, G, H, I, L, K, M, F, P, S, T, W, Y, V;
W167A, D, R, N, C, E, Q, G, H, I, L, K, M, F, P, S, T, Y, V;
D168A, R, N, C, E, Q, G, H, I, L, K, M, F, P, S, T, W, Y, V;
25 Q169A, D, R, N, C, E, G, H, I, L, K, M, F, P, S, T, W, Y, V;
S170A, D, R, N, C, E, Q, G, H, I, L, K, M, F, P, T, W, Y, V;
R171A, D, N, C, E, Q, G, H, I, L, K, M, F, P, S, T, W, Y, V;
Q172A, D, R, N, C, E, G, H, I, L, K, M, F, P, S, T, W, Y, V;
F173A, D, R, N, C, E, Q, G, H, I, L, K, M, P, S, T, W, Y, V;
30 Q174*, A, D, R, N, C, E, G, H, I, L, K, M, F, P, S, T, W, Y, V;
D183*, A, D, R, N, C, E, Q, G, H, I, L, K, M, F, P, S, W, Y, V;
G184*, A, R, N, C, E, Q, G, H, I, L, K, M, F, P, S, T, W, Y, V;
N195A, D, R, C, E, Q, G, H, I, L, K, M, F, P, S, T, W, Y, V;
F267A, D, R, N, C, E, Q, G, H, I, L, K, M, P, S, T, W, Y, V;
35 W268A, D, R, N, C, E, Q, G, H, I, L, K, M, F, P, S, T, Y, V;
K269A, D, R, N, C, E, Q, G, H, I, L, M, F, P, S, T, W, Y, V;
N270A, D, R, C, E, Q, G, H, I, L, K, M, F, P, S, T, W, Y, V;

D271A, R, N, C, E, Q, G, H, I, L, K, M, F, P, S, T, W, Y, V;
L272A, D, R, N, C, E, Q, G, H, I, K, M, F, P, S, T, W, Y, V;
G273A, D, R, N, C, E, Q, H, I, L, K, M, F, P, S, T, W, Y, V;
A274D, R, N, C, E, Q, G, H, I, L, K, M, F, P, S, T, W, Y, V;
5 L275A, D, R, N, C, E, Q, G, H, I, K, M, F, P, S, T, W, Y, V;
G456A, D, R, N, C, E, Q, H, I, L, K, M, F, P, S, T, W, Y, V;
N457A, D, R, C, E, Q, G, H, I, L, K, M, F, P, S, T, W, Y, V;
K458A, D, R, N, C, E, Q, G, H, I, L, M, F, P, S, T, W, Y, V;
P459A, D, R, N, C, E, Q, G, H, I, L, K, M, F, S, T, W, Y, V;
10 G460A, D, R, N, C, E, Q, H, I, L, K, M, F, P, S, T, W, Y, V;
T461A, D, R, N, C, E, Q, G, H, I, L, K, M, F, P, S, W, Y, V;
V462A, D, R, N, C, E, Q, G, H, I, L, K, M, F, P, S, T, W, Y;
T463A, D, R, N, C, E, Q, G, H, I, L, K, M, F, P, S, W, Y, V.

15 15. The variant according to claim 14, wherein the variant has one or more of the following substitutions or deletions:
Q174*, D183*, G184*, N195F, K269S.

16. The variant according to claims 13-15, wherein the parent
20 Termamyl-like α -amylase is the *B. licheniformis* α -amylase having the sequence shown in SEQ ID NO: 4.

17. A DNA construct comprising a DNA sequence encoding an α -
amylase variant according to any one of claims 1-16.

25

18. A recombinant expression vector which carries a DNA construct according to claim 17.

19. A cell which is transformed with a DNA construct according
30 to claim 17 or a vector according to claim 18.

20. A cell according to claim 19, which is a microorganism.

21. A cell according to claim 20, which is a bacterium or a
35 fungus.

22. The cell according to claim 21, which is a Gram positive bacterium such as *Bacillus subtilis*, *Bacillus licheniformis*,

Bacillus lentus, *Bacillus brevis*, *Bacillus stearothermophilus*, *Bacillus alkalophilus*, *Bacillus amyloliquefaciens*, *Bacillus coagulans*, *Bacillus circulans*, *Bacillus lautus* or *Bacillus thuringiensis*.

5

23. Use of an α -amylase variant according to any one of claims 1-16 for washing and/or dishwashing.

10

24. A detergent additive comprising an α -amylase variant according to any one of claims 1-16, optionally in the form of a non-dusting granulate, stabilized liquid or protected enzyme.

25. A detergent additive according to claim 24 which contains 0.02-200 mg of enzyme protein/g of the additive.

15

26. A detergent additive according to claims 24 or 25, which additionally comprises another enzyme such as a protease, a lipase, a peroxidase, another amylolytic enzyme and/or a cellulase.

20

27. A detergent composition comprising an α -amylase variant according to any of claims 1-16.

25

28. A detergent composition according to claim 27 which additionally comprises another enzyme such as a protease, a lipase, a peroxidase, another amylolytic enzyme and/or a cellulase.

30

29. A manual or automatic dishwashing detergent composition comprising an α -amylase variant according to any one of claims 1-16.

35

30. A dishwashing detergent composition according to claim 29 which additionally comprises another enzyme such as a protease, a lipase, a peroxidase, another amylolytic enzyme and/or a cellulase.

31. A manual or automatic laundry washing composition comprising

an α -amylase variant according to any one of claims 1-16.

32. A laundry washing composition according to claim 31, which additionally comprises another enzyme such as a protease, a
5 lipase, a peroxidase, an amylolytic enzyme and/or a cellulase.

33. Method for providing α -amylases with

1) altered pH optimum, and/or

2) altered temperature optimum, and/or

10 3) improved stability,

comprising the following steps:

i) identifying (a) target position(s) and/or region(s) for
mutation of the α -amylase by comparing the molecular dynamics of
two or more α -amylase's 3D structures having substantially
15 different pH, temperature and/or stability profiles,
ii) substituting, adding and/or deleting one or more amino acids
in the identified position(s) and/or region(s).

34. The method according to claim 33, wherein a medium
20 temperature α -amylase is compared with a high temperature α -
amylase.

35. The method according to claim 33, wherein a low temperature
 α -amylase is compared with a medium or high temperature α -
25 amylase.

36. The method according to claims 33-35, wherein the α -amylases
are at least 70%, preferably 80%, up to 90%, such as up to 95%,
especially 95% homologous.

30

37. The method according to claim 36, wherein the α -amylases
compared are Termamyl-like α -amylases.

38. The method according to claim 28, wherein the α -amylases
35 compared are any of the α -amylases shown in SEQ ID NO: 1 to SEQ
ID NO: 8.

1	HHNGTNGTMM	QYFEWHL PND	GNHWNRLRDD	ASNLRNRGIT	AIWIPPAWK	50
1	..NGTNGTMM	QYFEWYLPND	GNHWNRLRSD	ASNLKDKGIS	AVWIPPAWK	
2	HHNGTNGTMM	QYFEWYLPND	GNHWNRLRDD	AANLKS KGIT	AVWIPPAWK	
3	...VNGTLM	QYFEWYTPND	GQHWKRLQND	AEHLSDIGIT	AVWIPPAYK	
4	..ANLNGTLM	QYFEWYMPND	GQHWRRRLQND	SAYLAEHGIT	AVWIPPAYK	
5	.AAPFNGTMM	QYFEWYLPDD	GTLWTKVANE	ANLSSLGIT	ALWLPAYK	
6						

51						100
1	TSQNDVGYGA	YDLYDLGEFN	QKGTVRTKYG	TRSQLESAIH	ALKNNGVQVY	
2	ASQNDVGYGA	YDLYDLGEFN	QKGTIRTKYG	TRNQLQAAVN	ALKSNGIQVY	
3	TSQNDVGYGA	YDLYDLGEFN	QKGTVRTKYG	TRNQLQAAVT	SLKNNGIQVY	
4	LSQSDNGYGP	YDLYDLGEFQ	QKGTVRTKYG	TKSELQDAIG	SLHSRNVQVY	
5	TSQADVGYGA	YDLYDLGEFH	QKGTVRTKYG	TKGELQSAIK	SLHSRDINVY	
6	TSRSDVGYGV	YDLYDLGEFN	QKGTVRTKYG	TKAQYLQAIQ	AAHAAGMQVY	

101							150
1	GDVVMNHKGG	ADATENVLAV	EVNPNNRNQE	ISGDYTIKAW	TKFDFPGRGN		
2	GDVVMNHKGG	ADATEMVRVAV	EVNPNNRNQE	VSGEYTIKAW	TKFDFPGRGN		
3	GDVVMNHKGG	ADGTEIVNAV	EVNRSNRNQE	TSGEYAIKAW	TKFDFPGRGN		
4	GDVVLNHHKAG	ADATEDVTAV	EVNPNNRNQE	TSEYQIKAW	TDFRFPGRGN		
5	GDVVINHHKGG	ADATEDVTAV	EVDPADRNRV	ISGEHLIKAW	THHFPPGRGS		
6	ADVVFDPHKKGG	ADGTEWVDAV	EVNPSDRNQE	ISGTYQIQAW	TKFDFPGRGN		

151				200
1	TYSDFKWRWY	HFDGVWDQDS	RQFQNRIYKF	RGDGKAWDWE
2	THSNFKWRWY	HFDGVWDQDS	RKLNNRIYKF	RGDGKAWDWE
3	NHSSFKWRWY	HFDGTDWDQDS	RQLQNKIYKF	RGDGKAWDWE
4	TYSDFKWHWY	HFDGADWDES	RKI.SRIYKF	RGEKAWDWE
5	TYSDFKWHWY	HFDGTDWDES	RKL.NRIYKF	..QGKAWDWE
6	TYSDFKWRWY	HFDGVWDWDES	RKL.SRIYKF	RGDGKAWDWE
201				250
1	LMYADVMDH	PEVVNELRRW	GEWYNTLNL	DGERIDAVKH
2	LMYADIDMDH	PEVVNELRNW	GVWYNTLGL	DGERIDAVKH
3	LMYADVMDH	PEVIHELNRW	GVWYNTLNL	DGERIDAVKH
4	LMYADVDDH	PDVVAETKKW	GIWYANELSL	DGERIDAAKH
5	LMYADIDYDH	PDVAAEIKRW	GTWYANELQL	DGERLDAVKH
6	LMYADLDMDH	PEVVTELKNW	GKWWYVNTTNI	DGERLDAVKH
251				300
1	THVRNATGKE	MFAVAEEFWKN	DLGALENYLN	KTNWNHNSVFD
2	IHVRSATGKN	MFAVAEEFWKN	DLGALENYLN	KTNWNHNSVFD
3	THVRNTTGKP	MFAVAEEFWKN	DLGALENYLN	KTSWNHNSAFD
4	QAVRQATGKE	MFTVAEYWQN	NAGKLENYLN	KTSFNQSVFD
5	NHVREKTGKE	MFTVAEYWQN	DLGALENYLN	KTNFNHNSVFD
6	SYVRSQTGKP	LFTVGEYWSY	DINKLHNYIT	KTDGTMSLFD

Fig. 1 (continued)

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301						350
1	SNSGGNYDMA	KLLNGTVVQK	HPMHA VTFVD	NHDSQPGESL	ESFVQEWFKP	
2	SKSGGNYDMR	QIFNGTVVQR	HPMHA VTFVD	NHDSQPEEAL	ESFVEEWFKP	
3	SNSGGYYDMR	NILNGSVVQK	HPTHA VTFVD	NHDSQPGEAL	ESFVQQWFKP	
4	SSQGGGYDMR	RLLDGTVVSR	HPEKA VTFVE	NHDTQPGQSL	ESTVQTWFKP	
5	STQGGGYDMR	KLLNGTVVSK	HPLKS VTFVD	NHDTQPGQSL	ESTVQTWFKP	
6	SKSGGA FDMR	TLMTNTLMKD	QPTLA VTFVD	NHDTQPGQAL	QSWVDPWFKP	
351						400
1	LAYALILTRE	QGYPSVFYGD	YYGIP THS..	.VPAMKAKID	PILEARQ NFA	
2	LAYALTLTRE	QGYPSVFYGD	YYGIP THG..	.VPAMKSKID	PILEARQ KYA	
3	LAYALVLTRE	QGYPSVFYGD	YYGIP THG..	.VPAMKSKID	PLLQARQ TFA	
4	LAYAFILTRE	SGYPQVFYGD	MYG TKGTSPK	EIPSLKDNIE	PILKARKEYA	
5	LAYAFILTRE	SGYPQVFYGD	MYG TKGDSQR	EIPALKHKIE	PILKARKQYA	
6	LAYAFILTRQ	EGYPCVFYGD	YYGIPQYN..	.IPSLKSKID	PLLIARRDYA	
401						450
1	YGTQHDYFDH	HNIIGWTREG	NTHPNSGLA	TIMSDGPGGE	KWMYVGQNKA	
2	YGRQN.....	
3	YGTQHDYFDH	HDIIGWTREG	NSSH PNSGLA	TIMSDGPGGN	KWMYVGKNKA	
4	YGPQHDYIDH	PDVIGWTREG	DSSAAKSGLA	ALITDGP GGS	KRMYAGLKNA	
5	YGAQHDYFDH	HDIVGWTREG	DSSVANSGLA	ALITDGP GGA	KRMYVGRQNA	
6	YGTQHDYLDH	SDIIGWTREG	GTEKPGSGLA	ALITDGP GGS	KWMYVGKQHA	

Fig.1 (continued)

	451			500
1	GQVWHDITGN	KPGTVTINAD	GWANFSVNGG	SVSIWVKR..
2
3	GQVWRDITGN	RTGTVTINAD	GWGNFSVNGG	SVSVWVKQ..
4	GETWYDITGN	RSDTVKIGSD	GWGEFHVNDG	SVSIYVQ...
5	GETWHDITGN	RSEPVVINSE	GWGEFHVNGG	SVSIYVQR..
6	GKVFYDLTGN	RSDTVTINSD	GWGEFKVNGG	SVSVWVPRKT
				TVSTIARPIT
	501		519	
1		
2		
3		
4		
5		
6	TRPWTGEFVR	WTEPRLVAW		

Fig. 1 (continued)

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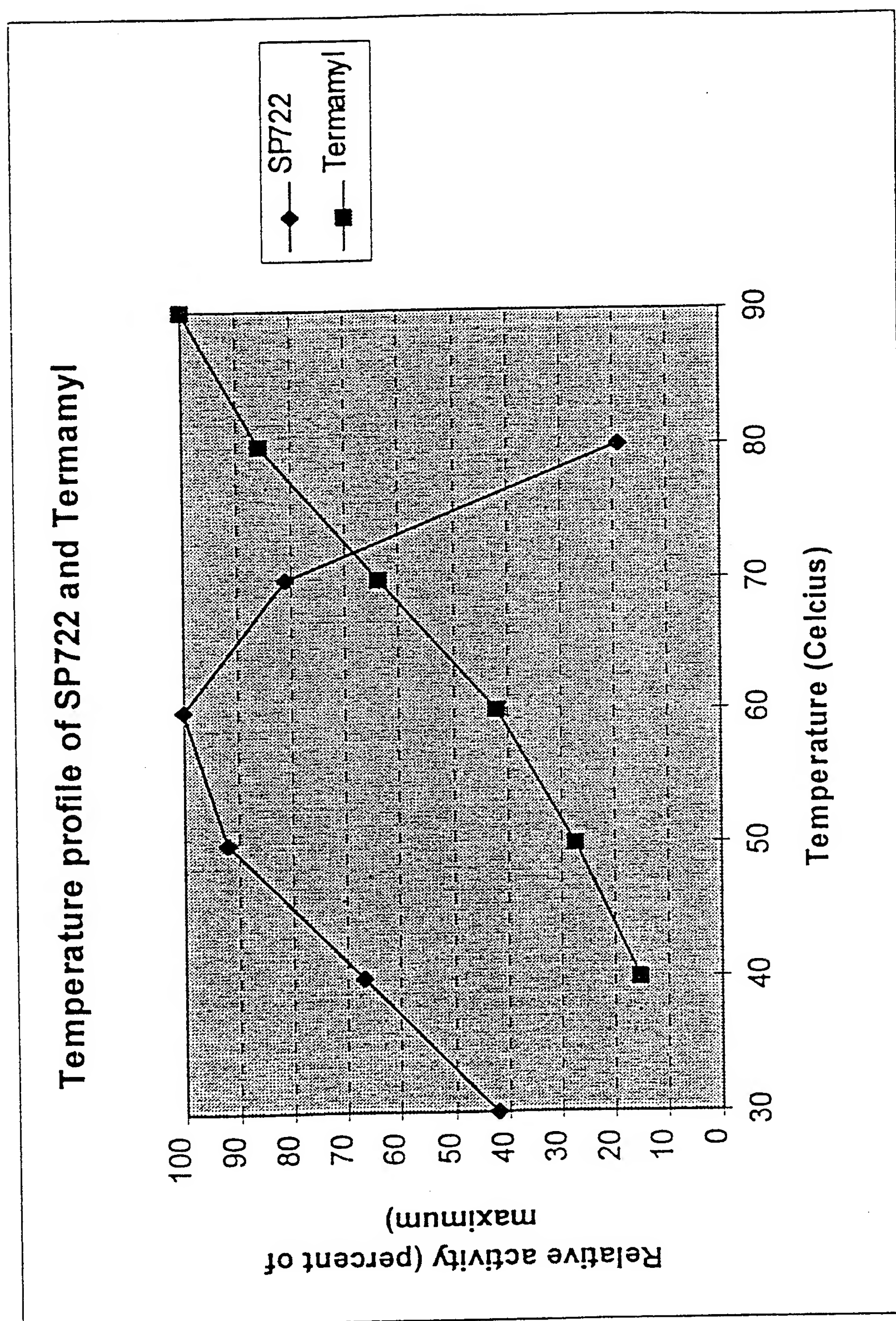


Fig. 2

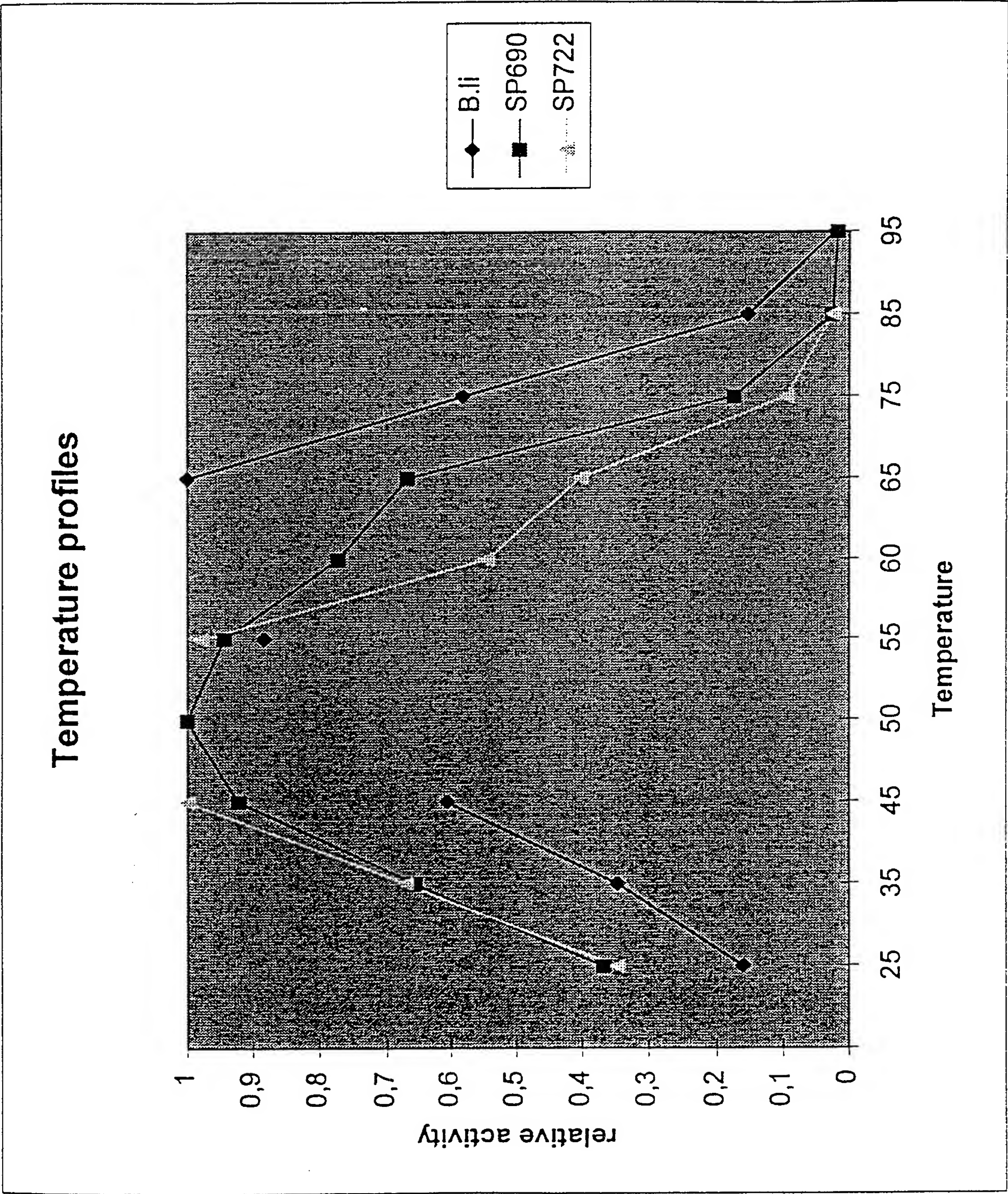


Fig. 3

1						50
1	MKFVLLLSLI	GFCWAQYDPH	TSDG.RTAIV	HLFEWRWVDI	AKECERYLAP	
2LLSLI	GFCWAQYDPH	TADG.RTAIV	HLFEWRWADI	AKECERYLAP	
3QYAPQ	TQSG.RTDIV	HLFEWRWVDI	ALECERYLGP	
4	MKFFLLLLFTI	GFCWAQYSPN	TQQG.RTSIV	HLFEWRWVDI	ALECERYLAP	
5	MKLNKIITTA	GLSLGLLLPS	IATATPTTFV	HLFEWNWQDV	AQECEQYLG	
51						100
1	KGFGGVQVSP	PNENVVHNP	SRPWERYQP	ISYKICTRSG	NEDEFRDMVT	
2	KGFGGVQVSP	PNENIIINNP	SRPWERYQP	ISYKICSRSG	NENEFKDMVT	
3	KGFGGVQVSP	PNENVVVTNP	SRPWERYQP	VSYKLCTRSG	NENEFRDMVT	
4	KGFGGVQVSP	PNENVAIYNP	FRPWERYQP	VSYKLCTRSG	NEDEFRNMVT	
5	KGYAAVQVSP	PNEHI....T	GSQWTRYQP	VSYELQSRGG	NRAQFIDMVN	
101						150
1	RCNNVGVRIY	VDAVINHMCG	AGNPAGTSST	CGSYLNPNNR	EFPAVPYSAW	
2	RCNNVGVRIY	VDAVINHMCG	SGNSAGTHST	CGSYFNPNNR	EFSAVPYSAW	
3	RCNNVGVRIY	VDAVINHMCG	SGAAAGTGTT	CGSYCNPGNR	EFPAVPYSAW	
4	RCNNVGVRIY	VDAVINHMCG	NAVSAGTSST	CGSYFNPGSR	DFPAVPYSGW	
5	RCSAAGVDIY	VDTLINHM..	.AAGSGTGTA	GNSF...GNK	SFPI..YSPQ	
151						200
1	DFNDNKN..	.GEIDNYNDA	YQVRNCRLTG	LLDLALEKDY	VRTKVADYMN	
2	YFNDNKN..	.GEINNYNDA	NQVRNCRLSG	LLDLALDKDY	VRTKVADYMN	
3	DFNDGKCKTA	SGGIESYNDP	YQVRDCQLVG	LLDLALEKDY	VRSMIADYLN	
4	DFNDGKCKTG	SGDIENYNDA	TQVRDCRLTG	LLDLALEKDY	VRSKIAEYMN	
5	DFHES.CTIN	NSDYG..NDR	YRVQNCCELVG	LADLDTASNY	VQNTIAAYIN	

Fig. 4

201	250
1 HLIDIGVAGF RLDAAKHMWP RDIKAVLDKL HNLNTKWFSQ GSRPFIQEV	
2 NLIDIGVAGF RLDAAKHMWP GDIKAVLDKL HNLNTKWFSQ GSRPFIQEV	
3 KLIDIGVAGF RLDASKHMWP GDIKAVLDKL HNLNTNWFPA GSRPFIQEV	
4 HLIDIGVAGF RLDASKHMWP GDIKAILDKL HNLNSNWFPA GSKPFIYQEV	
5 DLQAIGVKGF RFDASKHVAA SDIQSLMAKV N..... .GSPVVFQEV	
251	300
1 IDLGGEAIKG SEYFGNGRVT EFFYGAKLGT VIRKWNGEKM SYLKNWGEKW	
2 IDLGGEAIKG SEYFGNGRVT EFFYGAKLGT VIRKWNGEKM SYLKNWGEKW	
3 IDLGGEAIKS GEYFSNGRVT EFFYGAKLGT VVRKWSGEKM SYLKNWGEKW	
4 IDLGGEPIKS SDYFGNGRVT EFFYGAKLGT VIRKWNGEKM SYLKNWGEKW	
5 IDQGGGEAVGA SEYLSSTGLVT EFFYSTELGN TFR...NGSL AWLSNFGEKW	
301	350
1 GLVPSDRALV FVDNHDNQRG HGAGGSSILT FWDARMYKMA VGFMLAHPYG	
2 GFVPTDRALV FVDNHDNQRG HGAGGASILT FWDARMYKMA VGFMLAHPYG	
3 GFMPSDRALV FVDNHDNQRG HGAGGSSILT FWDAYRKLVA VGFMLAHPYG	
4 GFVPSDRALV FVDNHDNQRG HGAGGASILT FWDARLYKMA VGFMLAHPYG	
5 GFMPSSSAVV FVDNHDNQRG HGGAG.NVIT FEDGRLYDLA NVFMLAYPYG	

Fig. 4 (continued)

351400

1 FTRVMSSYRW NRNFQNGKDQ NDWIGPPNNN GVTKEVTINA DTTCGNDWVC

2 FTRVMSSYRR TRNFQNGKDV NDWIGPPNNN GVTKEVTINP DTTCGNDWVC

3 FTRVMSSYRW ARNFVNGEDV NDWIGPPNNN GVIKEVTINA DTTCGNDWVC

4 FTRVMSSYRW PRQFQNGNDV NDWVGPPNNN GVIKEVTINP DTTCGNDWVC

5 YPKVMSSY...DFHGDTDA GGPNVPVHNN GNLE.....CFASNWKC

401450

1 EHRWRQIRNM VAFRNVVNGQ .PFSNWWDDNN SNQVAFSRGN RGFI VFNNDD

2 EHRWRQIRNM VAFRNVVNGQ .PFANWWDDNG SNQVAFSRGN RGFI VFNNDD

3 EHRWREIRNM VWFRNVVDGE .PFANWWDDNG SNQVAFGRGN RGFI VFNNDD

4 EHRWRQIRNM VIFRNVVDGQ .PFTNWWDDNG SNQVAFGRGN RGFI VFNNDD

5 EHRWSYIAGG VDFRNNNTADN WAVTNWWDDNT NNQISFGRGS SGHMAINKE

451500

1 WALSATLQTG LPAGTYCDVI SGD KVDG..N CTGLRVNVGS DGKAHFSISN

2 WALSSTLQTG LPAGTYCDVI SGD KVN..N CTGLKVNVS DGKAHFSISN

3 WQLSSTLQTG LPAGTYCDVI SGD KVN..S CTGIKVYVSS DGKAQFSISN

4 WSFSLTLQTG LPAGTYCDVI SGD KING..N CTGIKIYVSD DGKAHFSISN

5 STL TATVQTD MASGQYCNVL KGELSADAKS CSGEVITVNS DGTINLNIGA

501521

1 SAEDPFI A I H ADSKL.....

2 SAEDPFI A I H ADSKL.....

3 SAEDPFI A I H AESKL.....

4 SAEDPFI A I H AESKL.....

5 WDA...MAI H KNAKLTSSA S

Fig. 4 (continued)

1
SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

5 (A) NAME: NOVO NORDISK A/S
 (B) STREET: Novo Alle
 (C) CITY: DK-2880 Bagsvaerd
 (E) COUNTRY: Denmark
 (F) POSTAL CODE (ZIP): DK-2880
 10 (G) TELEPHONE: +45 44 44 88 88
 (H) TELEFAX: +45 44 49 32 56
 (ii) TITLE OF INVENTION: α -amylase mutants
 (iii) NUMBER OF SEQUENCES: 46
 (iv) COMPUTER READABLE FORM:
 15 (A) MEDIUM TYPE: Floppy disk
 (B) COMPUTER: IBM PC compatible
 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 485 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 25 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

30 His His Asn Gly Thr Asn Gly Thr Met Met Gln Tyr Phe Glu Trp Tyr
 1 5 10 15
 Leu Pro Asn Asp Gly Asn His Trp Asn Arg Leu Arg Asp Asp Ala Ala
 20 25 30
 35 Asn Leu Lys Ser Lys Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Trp
 35 40 45
 Lys Gly Thr Ser Gln Asn Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr
 50 55 60
 40 Asp Leu Gly Glu Phe Asn Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly
 65 70 75 80
 Thr Arg Asn Gln Leu Gln Ala Ala Val Thr Ser Leu Lys Asn Asn Gly
 45 85 90 95
 Ile Gln Val Tyr Gly Asp Val Val Met Asn His Lys Gly Gly Ala Asp
 100 105 110
 50 Gly Thr Glu Ile Val Asn Ala Val Glu Val Asn Arg Ser Asn Arg Asn
 115 120 125
 Gln Glu Thr Ser Gly Glu Tyr Ala Ile Glu Ala Trp Thr Lys Phe Asp
 130 135 140
 55 Phe Pro Gly Arg Gly Asn Asn His Ser Ser Phe Lys Trp Arg Trp Tyr
 145 150 155 160

	His Phe Asp Gly Thr Asp Trp Asp Gln Ser Arg Gln Leu Gln Asn Lys	
	165	170 175
5	Ile Tyr Lys Phe Arg Gly Thr Gly Lys Ala Trp Asp Trp Glu Val Asp	
	180	185 190
	Thr Glu Asn Gly Asn Tyr Asp Tyr Leu Met Tyr Ala Asp Val Asp Met	
	195	200 205
10	Asp His Pro Glu Val Ile His Glu Leu Arg Asn Trp Gly Val Trp Tyr	
	210	215 220
	Thr Asn Thr Leu Asn Leu Asp Gly Phe Arg Ile Asp Ala Val Lys His	
15	225	230 235 240
	Ile Lys Tyr Ser Phe Thr Arg Asp Trp Leu Thr His Val Arg Asn Thr	
	245	250 255
20	Thr Gly Lys Pro Met Phe Ala Val Ala Glu Phe Trp Lys Asn Asp Leu	
	260	265 270
	Gly Ala Ile Glu Asn Tyr Leu Asn Lys Thr Ser Trp Asn His Ser Val	
	275	280 285
25	Phe Asp Val Pro Leu His Tyr Asn Leu Tyr Asn Ala Ser Asn Ser Gly	
	290	295 300
	Gly Tyr Tyr Asp Met Arg Asn Ile Leu Asn Gly Ser Val Val Gln Lys	
30	305	310 315 320
	His Pro Thr His Ala Val Thr Phe Val Asp Asn His Asp Ser Gln Pro	
	325	330 335
35	Gly Glu Ala Leu Glu Ser Phe Val Gln Gln Trp Phe Lys Pro Leu Ala	
	340	345 350
	Tyr Ala Leu Val Leu Thr Arg Glu Gln Gly Tyr Pro Ser Val Phe Tyr	
	355	360 365
40	Gly Asp Tyr Tyr Gly Ile Pro Thr His Gly Val Pro Ala Met Lys Ser	
	370	375 380
	Lys Ile Asp Pro Leu Leu Gln Ala Arg Gln Thr Phe Ala Tyr Gly Thr	
45	385	390 395 400
	Gln His Asp Tyr Phe Asp His His Asp Ile Ile Gly Trp Thr Arg Glu	
	405	410 415
50	Gly Asn Ser Ser His Pro Asn Ser Gly Leu Ala Thr Ile Met Ser Asp	
	420	425 430
	Gly Pro Gly Gly Asn Lys Trp Met Tyr Val Gly Lys Asn Lys Ala Gly	
	435	440 445
55	Gln Val Trp Arg Asp Ile Thr Gly Asn Arg Thr Gly Thr Val Thr Ile	
	450	455 460

3

Asn Ala Asp Gly Trp Gly Asn Phe Ser Val Asn Gly Gly Ser Val Ser
 465 470 475 480

Val Trp Val Lys Gln
 485

5

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 485 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

10

15

His His Asn Gly Thr Asn Gly Thr Met Met Gln Tyr Phe Glu Trp His
 1 5 10 15

20

Leu Pro Asn Asp Gly Asn His Trp Asn Arg Leu Arg Asp Asp Ala Ser
 20 25 30

Asn Leu Arg Asn Arg Gly Ile Thr Ala Ile Trp Ile Pro Pro Ala Trp
 35 40 45

25

Lys Gly Thr Ser Gln Asn Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr
 50 55 60

Asp Leu Gly Glu Phe Asn Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly
 65 70 75 80

30

Thr Arg Ser Gln Leu Glu Ser Ala Ile His Ala Leu Lys Asn Asn Gly
 85 90 95

35

Val Gln Val Tyr Gly Asp Val Val Met Asn His Lys Gly Gly Ala Asp
 100 105 110

Ala Thr Glu Asn Val Leu Ala Val Glu Val Asn Pro Asn Asn Arg Asn
 115 120 125

40

Gln Glu Ile Ser Gly Asp Tyr Thr Ile Glu Ala Trp Thr Lys Phe Asp
 130 135 140

Phe Pro Gly Arg Gly Asn Thr Tyr Ser Asp Phe Lys Trp Arg Trp Tyr
 145 150 155 160

45

His Phe Asp Gly Val Asp Trp Asp Gln Ser Arg Gln Phe Gln Asn Arg
 165 170 175

50

Ile Tyr Lys Phe Arg Gly Asp Gly Lys Ala Trp Asp Trp Glu Val Asp
 180 185 190

Ser Glu Asn Gly Asn Tyr Asp Tyr Leu Met Tyr Ala Asp Val Asp Met
 195 200 205

55

Asp His Pro Glu Val Val Asn Glu Leu Arg Arg Trp Gly Glu Trp Tyr
 210 215 220

Thr Asn Thr Leu Asn Leu Asp Gly Phe Arg Ile Asp Ala Val Lys His

[illegible]

(2) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 514 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

	Ala	Ala	Pro	Phe	Asn	Gly	Thr	Met	Met	Gln	Tyr	Phe	Glu	Trp	Tyr	Leu	
	1				5					10					15		
5	Pro	Asp	Asp	Gly	Thr	Leu	Trp	Thr	Lys	Val	Ala	Asn	Glu	Ala	Asn	Asn	
				20					25					30			
	Leu	Ser	Ser	Leu	Gly	Ile	Thr	Ala	Leu	Trp	Leu	Pro	Pro	Ala	Tyr	Lys	
			35					40					45				
10	Gly	Thr	Ser	Arg	Ser	Asp	Val	Gly	Tyr	Gly	Val	Tyr	Asp	Leu	Tyr	Asp	
		50					55					60					
	Leu	Gly	Glu	Phe	Asn	Gln	Lys	Gly	Ala	Val	Arg	Thr	Lys	Tyr	Gly	Thr	
15	65					70					75					80	
	Lys	Ala	Gln	Tyr	Leu	Gln	Ala	Ile	Gln	Ala	Ala	His	Ala	Ala	Gly	Met	
					85					90					95		
20	Gln	Val	Tyr	Ala	Asp	Val	Val	Phe	Asp	His	Lys	Gly	Gly	Ala	Asp	Gly	
				100					105					110			
	Thr	Glu	Trp	Val	Asp	Ala	Val	Glu	Val	Asn	Pro	Ser	Asp	Arg	Asn	Gln	
			115					120					125				
25	Glu	Ile	Ser	Gly	Thr	Tyr	Gln	Ile	Gln	Ala	Trp	Thr	Lys	Phe	Asp	Phe	
		130					135					140					
	Pro	Gly	Arg	Gly	Asn	Thr	Tyr	Ser	Ser	Phe	Lys	Trp	Arg	Trp	Tyr	His	
30	145					150					155					160	
	Phe	Asp	Gly	Val	Asp	Trp	Asp	Glu	Ser	Arg	Lys	Leu	Ser	Arg	Ile	Tyr	
					165					170					175		
35	Lys	Phe	Arg	Gly	Ile	Gly	Lys	Ala	Trp	Asp	Trp	Glu	Val	Asp	Thr	Glu	
				180					185					190			
	Asn	Gly	Asn	Tyr	Asp	Tyr	Leu	Met	Tyr	Ala	Asp	Leu	Asp	Met	Asp	His	
			195					200					205				
40	Pro	Glu	Val	Val	Thr	Glu	Leu	Lys	Ser	Trp	Gly	Lys	Trp	Tyr	Val	Asn	
		210					215					220					
	Thr	Thr	Asn	Ile	Asp	Gly	Phe	Arg	Leu	Asp	Ala	Val	Lys	His	Ile	Lys	
45	225					230					235					240	
	Phe	Ser	Phe	Phe	Pro	Asp	Trp	Leu	Ser	Asp	Val	Arg	Ser	Gln	Thr	Gly	
					245					250					255		
50	Lys	Pro	Leu	Phe	Thr	Val	Gly	Glu	Tyr	Trp	Ser	Tyr	Asp	Ile	Asn	Lys	
				260					265					270			
	Leu	His	Asn	Tyr	Ile	Met	Lys	Thr	Asn	Gly	Thr	Met	Ser	Leu	Phe	Asp	
			275					280					285				
55	Ala	Pro	Leu	His	Asn	Lys	Phe	Tyr	Thr	Ala	Ser	Lys	Ser	Gly	Gly	Thr	
							295					300					

6

Phe Asp Met Arg Thr Leu Met Thr Asn Thr Leu Met Lys Asp Gln Pro
 305 310 315 320
 Thr Leu Ala Val Thr Phe Val Asp Asn His Asp Thr Glu Pro Gly Gln
 5 325 330 335
 Ala Leu Gln Ser Trp Val Asp Pro Trp Phe Lys Pro Leu Ala Tyr Ala
 340 345 350
 Phe Ile Leu Thr Arg Gln Glu Gly Tyr Pro Cys Val Phe Tyr Gly Asp
 10 355 360 365
 Tyr Tyr Gly Ile Pro Gln Tyr Asn Ile Pro Ser Leu Lys Ser Lys Ile
 15 370 375 380
 Asp Pro Leu Leu Ile Ala Arg Arg Asp Tyr Ala Tyr Gly Thr Gln His
 385 390 395 400
 Asp Tyr Leu Asp His Ser Asp Ile Ile Gly Trp Thr Arg Glu Gly Val
 20 405 410 415
 Thr Glu Lys Pro Gly Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro
 420 425 430
 Gly Gly Ser Lys Trp Met Tyr Val Gly Lys Gln His Ala Gly Lys Val
 25 435 440 445
 Phe Tyr Asp Leu Thr Gly Asn Arg Ser Asp Thr Val Thr Ile Asn Ser
 450 455 460
 Asp Gly Trp Gly Glu Phe Lys Val Asn Gly Gly Ser Val Ser Val Trp
 30 465 470 475 480
 Val Pro Arg Lys Thr Thr Val Ser Thr Ile Ala Trp Ser Ile Thr Thr
 35 485 490 495
 Arg Pro Trp Thr Asp Glu Phe Val Arg Trp Thr Glu Pro Arg Leu Val
 500 505 510
 Ala Trp
 40

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 483 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Ala Asn Leu Asn Gly Thr Leu Met Gln Tyr Phe Glu Trp Tyr Met Pro
 1 5 10 15

55 Asn Asp Gly Gln His Trp Arg Arg Leu Gln Asn Asp Ser Ala Tyr Leu
 20 25 30

Ala Glu His Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly

7

	35	40	45
	Thr Ser Gln Ala Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr Asp Leu		
	50	55	60
5	Gly Glu Phe His Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys		
	65	70	75 80
	Gly Glu Leu Gln Ser Ala Ile Lys Ser Leu His Ser Arg Asp Ile Asn		
10		85	90 95
	Val Tyr Gly Asp Val Val Ile Asn His Lys Gly Gly Ala Asp Ala Thr		
	100	105	110
15	Glu Asp Val Thr Ala Val Glu Val Asp Pro Ala Asp Arg Asn Arg Val		
	115	120	125
	Ile Ser Gly Glu His Leu Ile Lys Ala Trp Thr His Phe His Phe Pro		
20	130	135	140
	Gly Arg Gly Ser Thr Tyr Ser Asp Phe Lys Trp His Trp Tyr His Phe		
	145	150	155 160
	Asp Gly Thr Asp Trp Asp Glu Ser Arg Lys Leu Asn Arg Ile Tyr Lys		
25		165	170 175
	Phe Gln Gly Lys Ala Trp Asp Trp Glu Val Ser Asn Glu Asn Gly Asn		
	180	185	190
30	Tyr Asp Tyr Leu Met Tyr Ala Asp Ile Asp Tyr Asp His Pro Asp Val		
	195	200	205
	Ala Ala Glu Ile Lys Arg Trp Gly Thr Trp Tyr Ala Asn Glu Leu Gln		
35	210	215	220
	Leu Asp Gly Phe Arg Leu Asp Ala Val Lys His Ile Lys Phe Ser Phe		
	225	230	235 240
	Leu Arg Asp Trp Val Asn His Val Arg Glu Lys Thr Gly Lys Glu Met		
40		245	250 255
	Phe Thr Val Ala Glu Tyr Trp Gln Asn Asp Leu Gly Ala Leu Glu Asn		
	260	265	270
45	Tyr Leu Asn Lys Thr Asn Phe Asn His Ser Val Phe Asp Val Pro Leu		
	275	280	285
	His Tyr Gln Phe His Ala Ala Ser Thr Gln Gly Gly Gly Tyr Asp Met		
50	290	295	300
	Arg Lys Leu Leu Asn Gly Thr Val Val Ser Lys His Pro Leu Lys Ser		
	305	310	315 320
	Val Thr Phe Val Asp Asn His Asp Thr Gln Pro Gly Gln Ser Leu Glu		
55		325	330 335
	Ser Thr Val Gln Thr Trp Phe Lys Pro Leu Ala Tyr Ala Phe Ile Leu		
	340	345	350

Thr Arg Glu Ser Gly Tyr Pro Gln Val Phe Tyr Gly Asp Met Tyr Gly
 355 360 365
 5 Thr Lys Gly Asp Ser Gln Arg Glu Ile Pro Ala Leu Lys His Lys Ile
 370 375 380
 Glu Pro Ile Leu Lys Ala Arg Lys Gln Tyr Ala Tyr Gly Ala Gln His
 385 390 395 400
 10 Asp Tyr Phe Asp His His Asp Ile Val Gly Trp Thr Arg Glu Gly Asp
 405 410 415
 Ser Ser Val Ala Asn Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro
 420 425 430
 Gly Gly Ala Lys Arg Met Tyr Val Gly Arg Gln Asn Ala Gly Glu Thr
 435 440 445
 20 Trp His Asp Ile Thr Gly Asn Arg Ser Glu Pro Val Val Ile Asn Ser
 450 455 460
 Glu Gly Trp Gly Glu Phe His Val Asn Gly Gly Ser Val Ser Ile Tyr
 465 470 475 480
 25 Val Gln Arg

(2) INFORMATION FOR SEQ ID NO: 5:

30 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 480 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

Val Asn Gly Thr Leu Met Gln Tyr Phe Glu Trp Tyr Thr Pro Asn Asp
 1 5 10 15
 40 Gly Gln His Trp Lys Arg Leu Gln Asn Asp Ala Glu His Leu Ser Asp
 20 25 30
 Ile Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly Leu Ser
 35 40 45
 45 Gln Ser Asp Asn Gly Tyr Gly Pro Tyr Asp Leu Tyr Asp Leu Gly Glu
 50 55 60
 50 Phe Gln Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys Ser Glu
 65 70 75 80
 Leu Gln Asp Ala Ile Gly Ser Leu His Ser Arg Asn Val Gln Val Tyr
 85 90 95
 55 Gly Asp Val Val Leu Asn His Lys Ala Gly Ala Asp Ala Thr Glu Asp
 100 105 110

Val Thr Ala Val Glu Val Asn Pro Ala Asn Arg Asn Gln Glu Thr Ser
115 120 125

5 Glu Glu Tyr Gln Ile Lys Ala Trp Thr Asp Phe Arg Phe Pro Gly Arg
 130 135 140

Gly Asn Thr Tyr Ser Asp Phe Lys Trp His Trp Tyr His Phe Asp Gly
145 150 155 160

10 Ala Asp Trp Asp Glu Ser Arg Lys Ile Ser Arg Ile Phe Lys Phe Arg
165 170 175

Gly Glu Gly Lys Ala Trp Asp Trp Glu Val Ser Ser Glu Asn Gly Asn
180 185 190

15 Tyr Asp Tyr Leu Met Tyr Ala Asp Val Asp Tyr Asp His Pro Asp Val
195 200 205

Val Ala Glu Thr Lys Lys Trp Gly Ile Trp Tyr Ala Asn Glu Leu Ser
20 210 215 220

Leu Asp Gly Phe Arg Ile Asp Ala Ala Lys His Ile Lys Phe Ser Phe
225 230 235 240

25 Leu Arg Asp Trp Val Gln Ala Val Arg Gln Ala Thr Gly Lys Glu Met
 245 250 255

Phe Thr Val Ala Glu Tyr Trp Gln Asn Asn Ala Gly Lys Leu Glu Asn
260 265 270

30 Tyr Leu Asn Lys Thr Ser Phe Asn Gln Ser Val Phe Asp Val Pro Leu
275 280 285

35 His Phe Asn Leu Gln Ala Ala Ser Ser Gln Gly Gly Gly Tyr Asp Met
290 295 300

Arg Arg Leu Leu Asp Gly Thr Val Val Ser Arg His Pro Glu Lys Ala
305 310 315 320

40 Val Thr Phe Val Glu Asn His Asp Thr Gln Pro Gly Gln Ser Leu Glu
325 330 335

Ser Thr Val Gln Thr Trp Phe Lys Pro Leu Ala Tyr Ala Phe Ile Leu
340 345 350

45
Thr Arg Glu Ser Gly Tyr Pro Gln Val Phe Tyr Gly Asp Met Tyr Gly
355 360 365

Thr Lys Gly Thr Ser Pro Lys Glu Ile Pro Ser Leu Lys Asp Asn Ile
50 370 375 380

Glu Pro Ile Leu Lys Ala Arg Lys Glu Tyr Ala Tyr Gly Pro Gln His
385 390 395 400

55 Asp Tyr Ile Asp His Pro Asp Val Ile Gly Trp Thr Arg Glu Gly Asp
405 410 415

Ser Ser Ala Ala Lys Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro

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(2) INFORMATION FOR SEQ ID NO: 6:
15   (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 485 amino acids
      (B) TYPE: amino acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear
20   (ii) MOLECULE TYPE: peptide
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

      His His Asn Gly Thr Asn Gly Thr Met Met Gln Tyr Phe Glu Trp Tyr
      1          5          10          15
25
      Leu Pro Asn Asp Gly Asn His Trp Asn Arg Leu Asn Ser Asp Ala Ser
      20          25          30
30
      Asn Leu Lys Ser Lys Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Trp
      35          40          45
      Lys Gly Ala Ser Gln Asn Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr
      50          55          60
35
      Asp Leu Gly Glu Phe Asn Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly
      65          70          75          80
      Thr Arg Ser Gln Leu Gln Ala Ala Val Thr Ser Leu Lys Asn Asn Gly
      85          90          95
40
      Ile Gln Val Tyr Gly Asp Val Val Met Asn His Lys Gly Gly Ala Asp
      100         105         110
45
      Ala Thr Glu Met Val Arg Ala Val Glu Val Asn Pro Asn Asn Arg Asn
      115         120         125
      Gln Glu Val Thr Gly Glu Tyr Thr Ile Glu Ala Trp Thr Arg Phe Asp
      130         135         140
50
      Phe Pro Gly Arg Gly Asn Thr His Ser Ser Phe Lys Trp Arg Trp Tyr
      145         150         155         160
      His Phe Asp Gly Val Asp Trp Asp Gln Ser Arg Arg Leu Asn Asn Arg
      165         170         175
55
      Ile Tyr Lys Phe Arg Gly His Gly Lys Ala Trp Asp Trp Glu Val Asp
      180         185         190

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[illegible]

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 485 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

10

His His Asn Gly Thr Asn Gly Thr Met Met Gln Tyr Phe Glu Trp Tyr
1 5 10 15

15

Leu Pro Asn Asp Gly Asn His Trp Asn Arg Leu Arg Asp Asp Ala Ala
20 25 30

Asn Leu Lys Ser Lys Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Trp
35 40 45

20

Lys Gly Thr Ser Gln Asn Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr
50 55 60

Asp Leu Gly Glu Phe Asn Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly
65 70 75 80

25

Thr Arg Asn Gln Leu Gln Ala Ala Val Thr Ser Leu Lys Asn Asn Gly
85 90 95

30

Ile Gln Val Tyr Gly Asp Val Val Met Asn His Lys Gly Gly Ala Asp
100 105 110

Gly Thr Glu Ile Val Asn Ala Val Glu Val Asn Arg Ser Asn Arg Asn
115 120 125

35

Gln Glu Thr Ser Gly Glu Tyr Ala Ile Glu Ala Trp Thr Lys Phe Asp
130 135 140

Phe Pro Gly Arg Gly Asn Asn His Ser Ser Phe Lys Trp Arg Trp Tyr
145 150 155 160

40

His Phe Asp Gly Thr Asp Trp Asp Gln Ser Arg Gln Leu Gln Asn Lys
165 170 175

45

Ile Tyr Lys Phe Arg Gly Thr Gly Lys Ala Trp Asp Trp Glu Val Asp
180 185 190

Thr Glu Asn Gly Asn Tyr Asp Tyr Leu Met Tyr Ala Asp Val Asp Met
195 200 205

50

Asp His Pro Glu Val Ile His Glu Leu Arg Asn Trp Gly Val Trp Tyr
210 215 220

Thr Asn Thr Leu Asn Leu Asp Gly Phe Arg Ile Asp Ala Val Lys His
225 230 235 240

55

Ile Lys Tyr Ser Phe Thr Arg Asp Trp Leu Thr His Val Arg Asn Thr
245 250 255

Thr Gly Lys Pro Met Phe Ala Val Ala Glu Phe Trp Lys Asn Asp Leu
260 265 270

Gly Ala Ile Glu Asn Tyr Leu Asn Lys Thr Ser Trp Asn His Ser Val
275 280 285

Phe Asp Val Pro Leu His Tyr Asn Leu Tyr Asn Ala Ser Asn Ser Gly
290 295 300

Gly Tyr Tyr Asp Met Arg Asn Ile Leu Asn Gly Ser Val Val Gln Lys
305 310 315 320

His Pro Thr His Ala Val Thr Phe Val Asp Asn His Asp Ser Gln Pro
325 330 335

Gly Glu Ala Leu Glu Ser Phe Val Gln Gln Trp Phe Lys Pro Leu Ala
340 345 350

Tyr Ala Leu Val Leu Thr Arg Glu Gln Gly Tyr Pro Ser Val Phe Tyr
355 360 365

Gly Asp Tyr Tyr Gly Ile Pro Thr His Gly Val Pro Ala Met Lys Ser
370 375 380

Lys Ile Asp Pro Leu Leu Gln Ala Arg Gln Thr Phe Ala Tyr Gly Thr
385 390 395 400

Gln His Asp Tyr Phe Asp His His Asp Ile Ile Gly Trp Thr Arg Glu
405 410 415

Gly Asn Ser Ser His Pro Asn Ser Gly Leu Ala Thr Ile Met Ser Asp
420 425 430

Gly Pro Gly Gly Asn Lys Trp Met Tyr Val Gly Lys Asn Lys Ala Gly
435 440 445

Gln Val Trp Arg Asp Ile Thr Gly Asn Arg Thr Gly Thr Val Thr Ile
450 455 460

Asn Ala Asp Gly Trp Gly Asn Phe Ser Val Asn Gly Gly Ser Val Ser
465 470 475 480

Val Trp Val Lys Gln
485

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 485 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

His His Asn Gly Thr Asn Gly Thr Met Met Gln Tyr Phe Glu Trp His
1 5 10 15

Leu Pro Asn Asp Gly Asn His Trp Asn Arg Leu Arg Asp Asp Ala Ser

	20	14 25	30
	Asn Leu Arg Asn Arg Gly Ile Thr Ala Ile Trp Ile Pro Pro Ala Trp		
	35	40	45
5	Lys Gly Thr Ser Gln Asn Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr		
	50	55	60
10	Asp Leu Gly Glu Phe Asn Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly		
	65	70	75
	Thr Arg Ser Gln Leu Glu Ser Ala Ile His Ala Leu Lys Asn Asn Gly		
	85	90	95
15	Val Gln Val Tyr Gly Asp Val Val Met Asn His Lys Gly Gly Ala Asp		
	100	105	110
	Ala Thr Glu Asn Val Leu Ala Val Glu Val Asn Pro Asn Asn Arg Asn		
	115	120	125
20	Gln Glu Ile Ser Gly Asp Tyr Thr Ile Glu Ala Trp Thr Lys Phe Asp		
	130	135	140
	Phe Pro Gly Arg Gly Asn Thr Tyr Ser Asp Phe Lys Trp Arg Trp Tyr		
25	145	150	155
	His Phe Asp Gly Val Asp Trp Asp Gln Ser Arg Gln Phe Gln Asn Arg		
	165	170	175
30	Ile Tyr Lys Phe Arg Gly Asp Gly Lys Ala Trp Asp Trp Glu Val Asp		
	180	185	190
	Ser Glu Asn Gly Asn Tyr Asp Tyr Leu Met Tyr Ala Asp Val Asp Met		
	195	200	205
35	Asp His Pro Glu Val Val Asn Glu Leu Arg Arg Trp Gly Glu Trp Tyr		
	210	215	220
	Thr Asn Thr Leu Asn Leu Asp Gly Phe Arg Ile Asp Ala Val Lys His		
40	225	230	235
	Ile Lys Tyr Ser Phe Thr Arg Asp Trp Leu Thr His Val Arg Asn Ala		
	245	250	255
45	Thr Gly Lys Glu Met Phe Ala Val Ala Glu Phe Trp Lys Asn Asp Leu		
	260	265	270
	Gly Ala Leu Glu Asn Tyr Leu Asn Lys Thr Asn Trp Asn His Ser Val		
	275	280	285
50	Phe Asp Val Pro Leu His Tyr Asn Leu Tyr Asn Ala Ser Asn Ser Gly		
	290	295	300
	Gly Asn Tyr Asp Met Ala Lys Leu Leu Asn Gly Thr Val Val Gln Lys		
55	305	310	315
	His Pro Met His Ala Val Thr Phe Val Asp Asn His Asp Ser Gln Pro		
	325	330	335

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E

(i) SEQUENCE CHARACTERISTICS:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1455 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

CATCATAATG GAACAAATGG TACTATGATG CAATATTTCTG AATGGTATTT GCCAAATGAC 60

GGGAATCATT GGAACAGGTT GAGGGATGAC GCAGCTAACT TAAAGAGTAA AGGGATAACA 120

GCTGTATGGA TCCCACCTGC ATGGAAGGGG ACTTCCCAGA ATGATGTAGG TTATGGAGCC 180

TATGATTTAT ATGATCTTGG AGAGTTTAAC CAGAAGGGGA CGGTTCGTAC AAAATATGGA 240

ACACGCAACC AGCTACAGGC TGCGGTGACC TCTTTAAAAA ATAACGGCAT TCAGGTATAT 300

GGTGATGTCG TCATGAATCA TAAAGGTGGA GCAGATGGTA CGGAAATTGT AAATGCGGTA 360

GAAGTGAATC GGAGCAACCG AAACCAGGAA ACCTCAGGAG AGTATGCAAT AGAAGCGTGG 420

ACAAAGTTTG ATTTTCCTGG AAGAGGAAAT AACCATTCCA GCTTTAAGTG GCGCTGGTAT 480

CATTTTGATG GGACAGATTG GGATCAGTCA CGCCAGCTTC AAAACAAAAT ATATAAATTC 540

16

AGGGGAACAG GCAAGGCCTG GGACTGGGAA GTCGATACAG AGAATGGCAA CTATGACTAT 600
CTTATGTATG CAGACGTGGA TATGGATCAC CCAGAAGTAA TACATGAACT TAGAAACTGG 660
5 GGAGTGTGGT ATACGAATAC ACTGAACCTT GATGGATTTA GAATAGATGC AGTGAAACAT 720
ATAAAATATA GCTTTACGAG AGATTGGCTT ACACATGTGC GTAACACCAC AGGTAAACCA 780
ATGTTTGCAG TGGCTGAGTT TTGGAAAAAT GACCTTGGTG CAATTGAAAA CTATTTGAAT 840
10 AAAACAAGTT GGAATCACTC GGTGTTTGAT GTTCCTCTCC ACTATAATTT GTACAATGCA 900
TCTAATAGCG GTGGTTATTA TGATATGAGA AATATTTTAA ATGGTTCTGT GGTGCAAAAA 960
15 CATCCAACAC ATGCCGTTAC TTTTGTGAT AACCATGATT CTCAGCCCGG GGAAGCATTG 1020
GAATCCTTTG TTCAACAATG GTTTAAACCA CTTGCATATG CATTGGTTCT GACAAGGGAA 1080
CAAGGTTATC CTTCCGTATT TTATGGGGAT TACTACGGTA TCCCAACCCA TGGTGTTCGG 1140
20 GCTATGAAAT CTAAAATAGA CCCTCTTCTG CAGGCACGTC AAACCTTTTG CTTATGGTACG 1200
CAGCATGATT ACTTTGATCA TCATGATATT ATCGGTTGGA CAAGAGAGGG AAATAGCTCC 1260
25 CATCCAAATT CAGGCCTTGC CACCATTATG TCAGATGGTC CAGGTGGTAA CAAATGGATG 1320
TATGTGGGGA AAAATAAAGC GGGACAAGTT TGGAGAGATA TTACCGGAAA TAGGACAGGC 1380
ACCGTCACAA TTAATGCAGA CGGATGGGGT AATTTCTCTG TTAATGGAGG GTCCGTTTCG 1440
30 GTTTGGGTGA AGCAA 1455

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 1455 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

CATCATAATG GGACAAATGG GACGATGATG CAATACTTTG AATGGCACTT GCCTAATGAT 60
GGGAATCACT GGAATAGATT AAGAGATGAT GCTAGTAATC TAAGAAATAG AGGTATAACC 120
45 GCTATTTGGA TTCCGCCTGC CTGGAAAGGG ACTTCGCAA ATGATGTGGG GTATGGAGCC 180
TATGATCTTT ATGATTTAGG GGAATTTAAT CAAAAGGGGA CGGTTCGTAC TAAGTATGGG 240
50 ACACGTAGTC AATTGGAGTC TGCCATCCAT GCTTTAAAGA ATAATGGCGT TCAAGTTTAT 300
GGGGATGTAG TGATGAACCA TAAAGGAGGA GCTGATGCTA CAGAAAACGT TCTTGCTGTC 360
GAGGTGAATC CAAATAACCG GAATCAAGAA ATATCTGGGG ACTACACAAT TGAGGCTTGG 420
55 ACTAAGTTTG ATTTTCCAGG GAGGGGTAAT ACATACTCAG ACTTTAAATG GCGTTGGTAT 480
CATTTGATG GTGTAGATTG GGATCAATCA CGACAATTCC AAAATCGTAT CTACAAATTC 540

CGAGGTGATG GTAAGGCATG GGATTGGGAA GTAGATTCGG AAAATGGAAA TTATGATTAT 600
 TTAATGTATG CAGATGTAGA TATGGATCAT CCGGAGGTAG TAAATGAGCT TAGAAGATGG 660
 5 GGAGAATGGT ATACAAATAC ATTAAATCTT GATGGATTTA GGATCGATGC GGTGAAGCAT 720
 ATTAAATATA GCTTTACACG TGATTGGTTG ACCCATGTAA GAAACGCAAC GGGAAAAGAA 780
 10 ATGTTTGCTG TTGCTGAATT TTGGAAAAAT GATTTAGGTG CCTTGGAGAA CTATTTAAAT 840
 AAAACAAACT GGAATCATTC TGTCTTTGAT GTCCCCCTTC ATTATAATCT TTATAACGCG 900
 TCAAATAGTG GAGGCAACTA TGACATGGCA AACTTCTTA ATGGAACGGT TGTTCAAAAG 960
 15 CATCCAATGC ATGCCGTAAC TTTTGTGGAT AATCACGATT CTCAACCTGG GGAATCATTA 1020
 GAATCATTTG TACAAGAATG GTTTAAGCCA CTTGCTTATG CGCTTATTTT AACAAGAGAA 1080
 20 CAAGGCTATC CCTCTGTCTT CTATGGTGAC TACTATGGAA TTCCAACACA TAGTGTCCCA 1140
 GCAATGAAAG CCAAGATTGA TCCAATCTTA GAGGCGCGTC AAAATTTTGC ATATGGAACA 1200
 CAACATGATT ATTTTGACCA TCATAATATA ATCGGATGGA CACGTGAAGG AAATACCACG 1260
 25 CATCCCAATT CAGGACTTGC GACTATCATG TCGGATGGGC CAGGGGGAGA GAAATGGATG 1320
 TACGTAGGGC AAAATAAAGC AGGTCAAGTT TGGCATGACA TAACTGGAAA TAAACCAGGA 1380
 30 ACAGTTACGA TCAATGCAGA TGGATGGGCT AATTTTTCAG TAAATGGAGG ATCTGTTTCC 1440
 ATTTGGGTGA AACGA 1455

- 35 (2) INFORMATION FOR SEQ ID NO: 11:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1548 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 40 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA (genomic)
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

GCCGCACCGT TTAACGGCAC CATGATGCAG TATTTTGAAT GGTACTTGCC GGATGATGGC 60
 45 ACGTTATGGA CCAAAGTGGC CAATGAAGCC AACAACTTAT CCAGCCTTGG CATCACCGCT 120
 CTTTGGCTGC CGCCCGCTTA CAAAGGAACA AGCCGCAGCG ACGTAGGGTA CGGAGTATAC 180
 50 GACTTGTATG ACCTCGGCGA ATTCAATCAA AAAGGGACCG TCCGCACAAA ATACGGAACA 240
 AAAGCTCAAT ATCTTCAAGC CATTCAAGCC GCCCACGCCG CTGGAATGCA AGTGTACGCC 300
 GATGTCGTGT TCGACCATAA AGGCGGCGCT GACGGCACGG AATGGGTGGA CGCCGTCGAA 360
 55 GTCAATCCGT CCGACCGCAA CCAAGAAATC TCGGGCACCT ATCAAATCCA AGCATGGACG 420
 AAATTTGATT TTCCCGGGCG GGGCAACACC TACTCCAGCT TTAAGTGGCG CTGGTACCAT 480

TTTGACGGCG TTGATTGGGA CGAAAGCCGA AAATTGAGCC GCATTTACAA ATTCCGCGGC 540
 ATCGGCAAAG CGTGGGATTG GGAAGTAGAC ACGGAAAACG GAAACTATGA CTACTTAATG 600
 5 TATGCCGACC TTGATATGGA TCATCCCGAA GTCGTGACCG AGCTGAAAAA CTGGGGGAAA 660
 TGGTATGTCA ACACAACGAA CATTGATGGG TTCCGGCTTG ATGCCGTCAA GCATATTAAG 720
 10 TTCAGTTTTT TTCCTGATTG GTTGTCGTAT GTGCGTTCTC AGACTGGCAA GCCGCTATTT 780
 ACCGTCGGGG AATATTGGAG CTATGACATC AACAAGTTGC ACAATTACAT TACGAAAACA 840
 GACGGAACGA TGTCTTTGTT TGATGCCCCG TTACACAACA AATTTTATAC CGCTTCCAAA 900
 15 TCAGGGGGCG CATTTGATAT GCGCACGTTA ATGACCAATA CTCTCATGAA AGATCAACCG 960
 ACATTGGCCG TCACCTTCGT TGATAATCAT GACACCGAAC CCGGCCAAGC GCTGCAGTCA 1020
 20 TGGGTCGACC CATGGTTCAA ACCGTTGGCT TACGCCTTTA TTCTAACTCG GCAGGAAGGA 1080
 TACCCGTGCG TCTTTTATGG TGACTATTAT GGCATTCCAC AATATAACAT TCCTTCGCTG 1140
 AAAAGCAAAA TCGATCCGCT CCTCATCGCG CGCAGGGATT ATGCTTACGG AACGCAACAT 1200
 25 GATTATCTTG ATCACTCCGA CATCATCGGG TGGACAAGGG AAGGGGGCAC TGAAAAACCA 1260
 GGATCCGGAC TGGCCGCACT GATCACCGAT GGGCCGGGAG GAAGCAAATG GATGTACGTT 1320
 30 GGCAAACAAC ACGCTGGAAA AGTGTTCTAT GACCTTACCG GCAACCGGAG TGACACCGTC 1380
 ACCATCAACA GTGATGGATG GGGGGAATTC AAAGTCAATG GCGGTTCCGT TTCGGTTTGG 1440
 GTTCCTAGAA AAACGACCGT TTCTACCATC GCTCGGCCGA TCACAACCCG ACCGTGGACT 1500
 35 GGTGAATTCG TCCGTTGGAC CGAACCACGG TTGGTGGCAT GGCCTTGA 1548

(2) INFORMATION FOR SEQ ID NO: 12:

- 40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1920 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 45 (ii) MOLECULE TYPE: DNA (genomic)
 (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 421..1872
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

50 CGGAAGATTG GAAGTACAAA AATAAGCAAA AGATTGTCAA TCATGTCATG AGCCATGCGG 60
 GAGACGGAAA AATCGTCTTA ATGCACGATA TTTATGCAAC GTTCGCAGAT GCTGCTGAAG 120
 55 AGATTATTAA AAAGCTGAAA GCAAAGGCT ATCAATTGGT AACTGTATCT CAGCTTGAAG 180
 AAGTGAAGAA GCAGAGAGGC TATTGAATAA ATGAGTAGAA GCGCCATATC GGCGCTTTTC 240

	TTTTGGAAGA AAATATAGGG AAAATGGTAC TTGTTAAAAA TTCGGAATAT TTATACAACA	300
	TCATATGTTT CACATTGAAA GGGGAGGAGA ATCATGAAAC AACAAAAACG GCTTTACGCC	360
5	CGATTGCTGA CGCTGTTATT TGCGCTCATC TTCTTGCTGC CTCATTCTGC AGCAGCGGCG	420
	GCA AAT CTT AAT GGG ACG CTG ATG CAG TAT TTT GAA TGG TAC ATG CCC	468
	AAT GAC GGC CAA CAT TGG AGG CGT TTG CAA AAC GAC TCG GCA TAT TTG	516
10	GCT GAA CAC GGT ATT ACT GCC GTC TGG ATT CCC CCG GCA TAT AAG GGA	564
	ACG AGC CAA GCG GAT GTG GGC TAC GGT GCT TAC GAC CTT TAT GAT TTA	612
15	GGG GAG TTT CAT CAA AAA GGG ACG GTT CGG ACA AAG TAC GGC ACA AAA	660
	GGA GAG CTG CAA TCT GCG ATC AAA AGT CTT CAT TCC CGC GAC ATT AAC	708
	GTT TAC GGG GAT GTG GTC ATC AAC CAC AAA GGC GGC GCT GAT GCG ACC	756
20	GAA GAT GTA ACC GCG GTT GAA GTC GAT CCC GCT GAC CGC AAC CGC GTA	804
	ATT TCA GGA GAA CAC CTA ATT AAA GCC TGG ACA CAT TTT CAT TTT CCG	852
25	GGG CGC GGC AGC ACA TAC AGC GAT TTT AAA TGG CAT TGG TAC CAT TTT	900
	GAC GGA ACC GAT TGG GAC GAG TCC CGA AAG CTG AAC CGC ATC TAT AAG	948
	TTT CAA GGA AAG GCT TGG GAT TGG GAA GTT TCC AAT GAA AAC GGC AAC	996
30	TAT GAT TAT TTG ATG TAT GCC GAC ATC GAT TAT GAC CAT CCT GAT GTC	1044
	GCA GCA GAA ATT AAG AGA TGG GGC ACT TGG TAT GCC AAT GAA CTG CAA	1092
35	TTG GAC GGT TTC CGT CTT GAT GCT GTC AAA CAC ATT AAA TTT TCT TTT	1140
	TTG CGG GAT TGG GTT AAT CAT GTC AGG GAA AAA ACG GGG AAG GAA ATG	1188
	TTT ACG GTA GCT GAA TAT TGG CAG AAT GAC TTG GGC GCG CTG GAA AAC	1236
40	TAT TTG AAC AAA ACA AAT TTT AAT CAT TCA GTG TTT GAC GTG CCG CTT	1284
	CAT TAT CAG TTC CAT GCT GCA TCG ACA CAG GGA GGC GGC TAT GAT ATG	1332
45	AGG AAA TTG CTG AAC GGT ACG GTC GTT TCC AAG CAT CCG TTG AAA TCG	1380
	GTT ACA TTT GTC GAT AAC CAT GAT ACA CAG CCG GGG CAA TCG CTT GAG	1428
	TCG ACT GTC CAA ACA TGG TTT AAG CCG CTT GCT TAC GCT TTT ATT CTC	1476
50	ACA AGG GAA TCT GGA TAC CCT CAG GTT TTC TAC GGG GAT ATG TAC GGG	1524
	ACG AAA GGA GAC TCC CAG CGC GAA ATT CCT GCC TTG AAA CAC AAA ATT	1572
55	GAA CCG ATC TTA AAA GCG AGA AAA CAG TAT GCG TAC GGA GCA CAG CAT	1620
	GAT TAT TTC GAC CAC CAT GAC ATT GTC GGC TGG ACA AGG GAA GGC GAC	1668

20

AGC TCG GTT GCA AAT TCA GGT TTG GCG GCA TTA ATA ACA GAC GGA CCC 1716
GGT GGG GCA AAG CGA ATG TAT GTC GGC CGG CAA AAC GCC GGT GAG ACA 1764
5 TGG CAT GAC ATT ACC GGA AAC CGT TCG GAG CCG GTT GTC ATC AAT TCG 1812
GAA GGC TGG GGA GAG TTT CAC GTA AAC GGC GGG TCG GTT TCA ATT TAT 1860
GTT CAA AGA TAG AAGAGCAGAG AGGACGGATT TCCTGAAGGA AATCCGTTTT 1912
10 TTTATTTT 1920

(2) INFORMATION FOR SEQ ID NO: 12:

15 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2084 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 343..1794

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

25 GCCCCGCACA TACGAAAAGA CTGGCTGAAA ACATTGAGCC TTTGATGACT GATGATTTGG 60
CTGAAGAAGT GGATCGATTG TTTGAGAAAA GAAGAAGACC ATAAAAATAC CTTGTCTGTC 120
30 ATCAGACAGG GTATTTTTTA TGCTGTCCAG ACTGTCCGCT GTGTAAAAAT AAGGAATAAA 180
GGGGGGTTGT TATTATTTTA CTGATATGTA AAATATAATT TGTATAAGAA AATGAGAGGG 240
AGAGGAAACA TGATTCAAAA ACGAAAGCGG ACAGTTTCGT TCAGACTTGT GCTTATGTGC 300
35 ACGCTGTTAT TTGTCAGTTT GCCGATTACA AAAACATCAG CC GTA AAT GGC ACG 354
CTG ATG CAG TAT TTT GAA TGG TAT ACG CCG AAC GAC GGC CAG CAT TGG 402
40 AAA CGA TTG CAG AAT GAT GCG GAA CAT TTA TCG GAT ATC GGA ATC ACT 450
GCC GTC TGG ATT CCT CCC GCA TAC AAA GGA TTG AGC CAA TCC GAT AAC 498
GGA TAC GGA CCT TAT GAT TTG TAT GAT TTA GGA GAA TTC CAG CAA AAA 546
45 GGG ACG GTC AGA ACG AAA TAC GGC ACA AAA TCA GAG CTT CAA GAT GCG 594
ATC GGC TCA CTG CAT TCC CGG AAC GTC CAA GTA TAC GGA GAT GTG GTT 642
50 TTG AAT CAT AAG GCT GGT GCT GAT GCA ACA GAA GAT GTA ACT GCC GTC 690
GAA GTC AAT CCG GCC AAT AGA AAT CAG GAA ACT TCG GAG GAA TAT CAA 738
ATC AAA GCG TGG ACG GAT TTT CGT TTT CCG GGC CGT GGA AAC ACG TAC 786
55 AGT GAT TTT AAA TGG CAT TGG TAT CAT TTC GAC GGA GCG GAC TGG GAT 834
GAA TCC CGG AAG ATC AGC CGC ATC TTT AAG TTT CGT GGG GAA GGA AAA 882

GCG TGG GAT TGG GAA GTA TCA AGT GAA AAC GGC AAC TAT GAC TAT TTA 930
 ATG TAT GCT GAT GTT GAC TAC GAC CAC CCT GAT GTC GTG GCA GAG ACA 978
 5 AAA AAA TGG GGT ATC TGG TAT GCG AAT GAA CTG TCA TTA GAC GGC TTC 1026
 CGT ATT GAT GCC GCC AAA CAT ATT AAA TTT TCA TTT CTG CGT GAT TGG 1074
 10 GTT CAG GCG GTC AGA CAG GCG ACG GGA AAA GAA ATG TTT ACG GTT GCG 1122
 GAG TAT TGG CAG AAT AAT GCC GGG AAA CTC GAA AAC TAC TTG AAT AAA 1170
 ACA AGC TTT AAT CAA TCC GTG TTT GAT GTT CCG CTT CAT TTC AAT TTA 1218
 15 CAG GCG GCT TCC TCA CAA GGA GGC GGA TAT GAT ATG AGG CGT TTG CTG 1266
 GAC GGT ACC GTT GTG TCC AGG CAT CCG GAA AAG GCG GTT ACA TTT GTT 1314
 20 GAA AAT CAT GAC ACA CAG CCG GGA CAG TCA TTG GAA TCG ACA GTC CAA 1362
 ACT TGG TTT AAA CCG CTT GCA TAC GCC TTT ATT TTG ACA AGA GAA TCC 1410
 GGT TAT CCT CAG GTG TTC TAT GGG GAT ATG TAC GGG ACA AAA GGG ACA 1458
 25 TCG CCA AAG GAA ATT CCC TCA CTG AAA GAT AAT ATA GAG CCG ATT TTA 1506
 AAA GCG CGT AAG GAG TAC GCA TAC GGG CCC CAG CAC GAT TAT ATT GAC 1554
 30 CAC CCG GAT GTG ATC GGA TGG ACG AGG GAA GGT GAC AGC TCC GCC GCC 1602
 AAA TCA GGT TTG GCC GCT TTA ATC ACG GAC GGA CCC GGC GGA TCA AAG 1650
 CGG ATG TAT GCC GGC CTG AAA AAT GCC GGC GAG ACA TGG TAT GAC ATA 1698
 35 ACG GGC AAC CGT TCA GAT ACT GTA AAA ATC GGA TCT GAC GGC TGG GGA 1746
 GAG TTT CAT GTA AAC GAT GGG TCC GTC TCC ATT TAT GTT CAG AAA TAA 1794
 40 GGTAATAAAA AAACACCTCC AAGCTGAGTG CGGGTATCAG CTTGGAGGTG CGTTTATTTT 1854
 TTCAGCCGTA TGACAAGGTC GGCATCAGGT GTGACAAATA CGGTATGCTG GCTGTCATAG 1914
 GTGACAAATC CGGGTTTTGC GCCGTTTGGC TTTTTCACAT GTCTGATTTT TGTATAATCA 1974
 45 ACAGGCACGG AGCCGGAATC TTTCGCCTTG GAAAAATAAG CGGCGATCGT AGCTGCTTCC 2034
 AATATGGATT GTTCATCGGG ATCGCTGCTT TTAATCACAA CGTGGGATCC 2084

50

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1455 base pairs

(B) TYPE: nucleic acid

55

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

CATCATAATG GAACAAATGG TACTATGATG CAATATTTTCG AATGGTATTT GCCAAATGAC 60
GGGAATCATT GGAACAGGTT GAGGGATGAC GCAGCTAACT TAAAGAGTAA AGGGATAACA 120
5 GCTGTATGGA TCCCACCTGC ATGGAAGGGG ACTTCCCAGA ATGATGTAGG TTATGGAGCC 180
TATGATTTAT ATGATCTTGG AGAGTTTAAAC CAGAAGGGGA CGGTTCGTAC AAAATATGGA 240
10 ACACGCAACC AGCTACAGGC TGCGGTGACC TCTTTAAAAA ATAACGGCAT TCAGGTATAT 300
GGTGATGTCTG TCATGAATCA TAAAGGTGGA GCAGATGGTA CGGAAATTGT AAATGCGGTA 360
GAAGTGAATC GGAGCAACCG AAACCAGGAA ACCTCAGGAG AGTATGCAAT AGAAGCGTGG 420
15 ACAAAGTTTG ATTTTCCTGG AAGAGGAAAT AACCATTCCA GCTTTAAGTG GCGCTGGTAT 480
CATTTTGATG GGACAGATTG GGATCAGTCA CGCCAGCTTC AAAACAAAAT ATATAAATTC 540
20 AGGGGAACAG GCAAGGCCTG GGAAGTGGAA GTCGATACAG AGAATGGCAA CTATGACTAT 600
CTTATGTATG CAGACGTGGA TATGGATCAC CCAGAAGTAA TACATGAACT TAGAAACTGG 660
GGAGTGTGGT ATACGAATAC ACTGAACCTT GATGGATTTA GAATAGATGC AGTGAAACAT 720
25 ATAAAATATA GCTTTACGAG AGATTGGCTT ACACATGTGC GTAACACCAC AGGTAAACCA 780
ATGTTTGCAG TGGCTGAGTT TTGGAAAAAT GACCTTGGTG CAATTGAAAA CTATTTGAAT 840
30 AAAACAAGTT GGAATCACTC GGTGTTTGAT GTTCCTCTCC ACTATAATTT GTACAATGCA 900
TCTAATAGCG GTGGTTATTA TGATATGAGA AATATTTTAA ATGGTTCTGT GGTGCAAAAA 960
CATCCAACAC ATGCCGTTAC TTTTGTTGAT AACCATGATT CTCAGCCCGG GGAAGCATTG 1020
35 GAATCCTTTG TTCAACAATG GTTTAAACCA CTTGCATATG CATTGGTTCT GACAAGGGAA 1080
CAAGGTTATC CTTCCGTATT TTATGGGGAT TACTACGGTA TCCCAACCCA TGGTGTTCGG 1140
40 GCTATGAAAT CTAAAATAGA CCCTCTTCTG CAGGCACGTC AAACTTTTCG CTATGGTACG 1200
CAGCATGATT ACTTTGATCA TCATGATATT ATCGGTTGGA CAAGAGAGGG AAATAGCTCC 1260
CATCCAAATT CAGGCCTTGC CACCATTATG TCAGATGGTC CAGGTGGTAA CAAATGGATG 1320
45 TATGTGGGGA AAAATAAAGC GGGACAAGTT TGGAGAGATA TTACCGGAAA TAGGACAGGC 1380
ACCGTCACAA TTAATGCAGA CGGATGGGGT AATTTCTCTG TTAATGGAGG GTCCGTTTCG 1440
50 GTTTGGGTGA AGCAA 1455

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1455 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

	CATCATAATG GGACAAATGG GACGATGATG CAATACTTTG AATGGCACTT GCCTAATGAT	60
5	GGGAATCACT GGAATAGATT AAGAGATGAT GCTAGTAATC TAAGAAATAG AGGTATAACC	120
	GCTATTTGGA TTCCGCCTGC CTGGAAAGGG ACTTCGCAA AATGATGTGGG GTATGGAGCC	180
	TATGATCTTT ATGATTTAGG GGAATTTAAT CAAAAGGGGA CGGTTCGTAC TAAGTATGGG	240
10	ACACGTAGTC AATTGGAGTC TGCCATCCAT GCTTTAAAGA ATAATGGCGT TCAAGTTTAT	300
	GGGGATGTAG TGATGAACCA TAAAGGAGGA GCTGATGCTA CAGAAAACGT TCTTGCTGTC	360
15	GAGGTGAATC CAAATAACCG GAATCAAGAA ATATCTGGGG ACTACACAAT TGAGGCTTGG	420
	ACTAAGTTTG ATTTTCCAGG GAGGGGTAAT ACATACTCAG ACTTTAAATG GCGTTGGTAT	480
	CATTTTCGATG GTGTAGATTG GGATCAATCA CGACAATTCC AAAATCGTAT CTACAAATTC	540
20	CGAGGTGATG GTAAGGCATG GGATTGGGAA GTAGATTCGG AAAATGGAAA TTATGATTAT	600
	TTAATGTATG CAGATGTAGA TATGGATCAT CCGGAGGTAG TAAATGAGCT TAGAAGATGG	660
25	GGAGAATGGT ATACAAATAC ATTAAATCTT GATGGATTTA GGATCGATGC GGTGAAGCAT	720
	ATTAAATATA GCTTTACACG TGATTGGTTG ACCCATGTAA GAAACGCAAC GGGAAAAGAA	780
	ATGTTTGCTG TTGCTGAATT TTGGAAAAAT GATTTAGGTG CCTTGGAGAA CTATTTAAAT	840
30	AAAACAAACT GGAATCATTC TGTCTTTGAT GTCCCCCTTC ATTATAATCT TTATAACGCG	900
	TCAAATAGTG GAGGCAACTA TGACATGGCA AACTTCTTA ATGGAACGGT TGTTCAAAAG	960
35	CATCCAATGC ATGCCGTAAC TTTTGTGGAT AATCACGATT CTCAACCTGG GGAATCATTA	1020
	GAATCATTTG TACAAGAATG GTTTAAGCCA CTTGCTTATG CGCTTATTTT AACAAGAGAA	1080
	CAAGGCTATC CCTCTGTCTT CTATGGTGAC TACTATGGAA TTCCAACACA TAGTGTCCCA	1140
40	GCAATGAAAG CCAAGATTGA TCCAATCTTA GAGGCGCGTC AAAATTTTGC ATATGGAACA	1200
	CAACATGATT ATTTTGACCA TCATAATATA ATCGGATGGA CACGTGAAGG AAATACCACG	1260
45	CATCCCAATT CAGGACTTGC GACTATCATG TCGGATGGGC CAGGGGGAGA GAAATGGATG	1320
	TACGTAGGGC AAAATAAAGC AGGTCAAGTT TGGCATGACA TAACTGGAAA TAAACCAGGA	1380
	ACAGTTACGA TCAATGCAGA TGGATGGGCT AATTTTTCAG TAAATGGAGG ATCTGTTTCC	1440
50	ATTTGGGTGA AACGA	1455

(2) INFORMATION FOR SEQ ID NO: 15:

- 55 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 60 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

24

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: other nucleic acid
(ix) FEATURE:
(A) NAME/ KEY: misc-feature:
5 (B) OTHER INFORMATION: /desc = "Forward Primer FSA"
(ix) FEATURE:
(A) NAME/KEY: misc-feature
(B) LOCATION: 22-27,29,31-33,41
(D): OTHER INFORMATION: /Note= 1: 35% A, 65% C
10 2: 83% G, 17% A
3: 63% G, 37% T
4: 86% G, 14% A
5: 85% G, 15% C
6: 50% T, 50% C
15 7: 95% A, 5%G
8: 58% G, 37% A, 5% T
9: 86% C, 13% A, 1% G
10: 83% T, 17% G
11: 92% G, 8% C
20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:
caaaatcgta tctacaaatt c123456a7g 8910tgggatt
11ggaagtaga ttcggaaaat
60
25 (2) INFORMATION FOR SEQ ID NO: 16:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
30 (C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: other nucleic acid
(ix) FEATURE:
(A) NAME/KEY: misc-feature:
35 (B) OTHER INFORMATION: /desc = "Reverse Primer RSA"
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:
gaatttgtag atacgatttt g
21
40 (2) INFORMATION FOR SEQ ID NO: 17:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
45 (B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: other nucleic acid
(ix) FEATURE:
50 (A) NAME/KEY: misc-feature:
(B) OTHER INFORMATION: /desc = "Primer B1"
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

CGATTGCTGA CGCTGTTATT TGCG

24

55

(2) INFORMATION FOR SEQ ID NO: 18:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs

25

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: other nucleic acid
 5 (ix) FEATURE:
 (A) NAME/KEY: misc-feature:
 (B) OTHER INFORMATION: /desc = "Primer Y2"
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

10 CTTGTTCCCT TGTCAGAACC AATG

24

(2) INFORMATION FOR SEQ ID NO: 19:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 base pairs
 15 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: other nucleic acid
 (ix) FEATURE:
 20 (A) NAME/KEY: misc-feature:
 (B) OTHER INFORMATION: /desc = "Primer 101458"
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

GTCATAGTTG CCGAAATCTG TATCGACTTC

30

25

(2) INFORMATION FOR SEQ ID NO: 20:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 35 base pairs
 30 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: other nucleic acid
 (ix) FEATURE:
 (A) NAME/KEY: misc-feature:
 35 (B) OTHER INFORMATION: /desc = "Primer 101638"
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

CCCAGTCCCA CGTACGTCCC CTGAATTTATATA TTTTG

35

40

(2) INFORMATION FOR SEQ ID NO: 21:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 45 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: other nucleic acid
 (ix) FEATURE:
 (A) NAME/KEY: misc-feature:
 (B) OTHER INFORMATION: /desc = "Oligo 1"
 50 (A) NAME/KEY: misc-feature
 (B) LOCATION: 12
 (D): OTHER INFORMATION: /Note=N= 25% A, 25% C, 25% G, 25% T.
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

55 CCCAGTCCCA GNTCTTTCCC CTGAATTTAT ATATTTTG

38

(2) INFORMATION FOR SEQ ID NO: 22:
 (i) SEQUENCE CHARACTERISTICS:

26

- (A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- 5 (ii) MOLECULE TYPE: other nucleic acid
(ix) FEATURE:
(A) NAME/KEY: misc-feature:
(B) OTHER INFORMATION: /desc = "Primer X2"
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

10

GCGTGGACAA AGTTTGATTT TCCTG

25

- (2) INFORMATION FOR SEQ ID NO: 23:
- 15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- 20 (ii) MOLECULE TYPE: other nucleic acid
(ix) FEATURE:
(A) NAME/KEY: misc-feature:
(B) OTHER INFORMATION: /desc = "Primer DA01"
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

25

- 2) INFORMATION FOR SEQ ID NO: 24:
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- 30 (ii) MOLECULE TYPE: other nucleic acid
(ix) FEATURE:
(A) NAME/KEY: misc-feature:
(B) OTHER INFORMATION: /desc = "Primer DA03"
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:
GCATTGGATG CTTTGAACA ACCG

24

- 2) INFORMATION FOR SEQ ID NO: 25:
- 40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- 45 (ii) MOLECULE TYPE: other nucleic acid
(ix) FEATURE:
(A) NAME/KEY: misc-feature:
(B) OTHER INFORMATION: /desc = "Primer DA07"
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

50

CGCAAAATGA TATCGGGTAT GGAGCC

26

- (2) INFORMATION FOR SEQ ID NO: 26:
- 55 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid

27

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: other nucleic acid
(ix) FEATURE:
5 (A) NAME/ KEY: misc-feature:
(B) OTHER INFORMATION: /desc = "Primer DA20"
(ix) FEATURE:
(A) NAME/KEY: misc-feature
(B) LOCATION: 13,14
10 (D): OTHER INFORMATION: /Note:S= mixture of C and G
W= mixture of A and T
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:
GTGATGAACC ACSWAGGTGG AGCTGATGC

29

15 (2) INFORMATION FOR SEQ ID NO: 27:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
20 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: other nucleic acid
(ix) FEATURE:
(A) NAME/ KEY: misc-feature:
(B) OTHER INFORMATION: /desc = "Primer DA14"
25 (ix) FEATURE:
(A) NAME/KEY: misc-feature
(B) LOCATION: 13,14
(D): OTHER INFORMATION: /Note:R= mixture of A and G
Y= mixture of C and T
30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:
GATGGTGTAT GGRYCAATCA CGACAATTCC

30

2) INFORMATION FOR SEQ ID NO: 28:
(i) SEQUENCE CHARACTERISTICS:
35 (A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: other nucleic acid
40 (ix) FEATURE:
(A) NAME/KEY: misc-feature:
(B) OTHER INFORMATION: /desc = "Primer DA15"
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:
GGTGTATGGG ATAACCTCAG ACAATTCC

28

45 2) INFORMATION FOR SEQ ID NO: 29:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28base pairs
(B) TYPE: nucleic acid
50 (C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: other nucleic acid
(ix) FEATURE:
(A) NAME/KEY: misc-feature:
55 (B) OTHER INFORMATION: /desc = "Primer DA16"

28

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:
GGTGTATGGG ATCTCTCACG ACAATTCC

28

2) INFORMATION FOR SEQ ID NO: 30:

5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
10 (ii) MOLECULE TYPE: other nucleic acid
(ix) FEATURE:
(A) NAME/KEY: misc-feature:
(B) OTHER INFORMATION: /desc = "Primer DA17"
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:
15 GGGATCAATC ACGAAATTTT CAAAATCGTA TC 32

2) INFORMATION FOR SEQ ID NO: 31:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 base pairs
20 (B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: other nucleic acid
(ix) FEATURE:
25 (A) NAME/KEY: misc-feature:
(B) OTHER INFORMATION: /desc = "Primer DA18"
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:
GGGATCAATC ACGACTCTTC CAAAATCGTA TC 32

30 2) INFORMATION FOR SEQ ID NO: 32:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 34 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
35 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: other nucleic acid
(ix) FEATURE:
(A) NAME/KEY: misc-feature:
(B) OTHER INFORMATION: /desc = "Primer DA06"
40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:
GGAAATTATG ATTATATCAT GTATGCAGAT GTAG 34

2) INFORMATION FOR SEQ ID NO: 33:

(i) SEQUENCE CHARACTERISTICS:
45 (A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: other nucleic acid
50 (ix) FEATURE:
(A) NAME/KEY: misc-feature:
(B) OTHER INFORMATION: /desc = "Primer DA09"
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:
GCTGAATTTT GGTCGAATGA TTTAGGTGCC 30

2) INFORMATION FOR SEQ ID NO: 34:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(ix) FEATURE:

(A) NAME/KEY: misc-feature:

(B) OTHER INFORMATION: /desc = "Primer DA11"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

GCTGAATTTT GGTCTGAATGA TTTAGGTGCC

30

2) INFORMATION FOR SEQ ID NO: 35:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(ix) FEATURE:

(A) NAME/KEY: misc-feature:

(B) OTHER INFORMATION: /desc = "Primer DA21"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

GAATTTTGGG AGTACGATTT AGGTCGG

27

(2) INFORMATION FOR SEQ ID NO: 36:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(ix) FEATURE:

(A) NAME/ KEY: misc-feature:

(B) OTHER INFORMATION: /desc = "Primer DA12"

(ix) FEATURE:

(A) NAME/KEY: misc-feature

(B) LOCATION: 12,13

(D): OTHER INFORMATION: /Note:R= mixture of A and G
Y= mixture of C and T

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

GGAAAAACGA TRYCGGTGCC TTGGAGAAC

29

(2) INFORMATION FOR SEQ ID NO: 37:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(ix) FEATURE:

(A) NAME/ KEY: misc-feature:

(B) OTHER INFORMATION: /desc = "Primer DA13"

30

(ix) FEATURE:

(A) NAME/KEY: misc-feature

(B) LOCATION: 14,15

(D): OTHER INFORMATION: /Note:R= mixture of A and G

Y= mixture of C and T

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37

GATTAGGTG CCTRYCAGAA CTATTTA

27

2) INFORMATION FOR SEQ ID NO: 38:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(ix) FEATURE:

(A) NAME/KEY: misc-feature:

(B) OTHER INFORMATION: /desc = "Primer DA08"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

CCCCCTTCAT GAGAATCTTT ATAACG

26

2) INFORMATION FOR SEQ ID NO: 39:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(ix) FEATURE:

(A) NAME/KEY: misc-feature:

(B) OTHER INFORMATION: /desc = "Primer DA04"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

GAATCCGAAC CTCATTACAC ATTCG

25

2) INFORMATION FOR SEQ ID NO: 40:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 38 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(ix) FEATURE:

(A) NAME/KEY: misc-feature:

(B) OTHER INFORMATION: /desc = "Primer DA05"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

CGGATGGACT CGAGAAGGAA ATACCACG

38

2) INFORMATION FOR SEQ ID NO: 41:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(ix) FEATURE:

31

(A) NAME/KEY: misc-feature:
(B) OTHER INFORMATION: /desc = "Primer DA10"
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:
CGTAGGGCAA AATCAGGCCG GTCAAGTTTG G 31

5

2) INFORMATION FOR SEQ ID NO: 42:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: other nucleic acid
(ix) FEATURE:

10

(A) NAME/KEY: misc-feature:
(B) OTHER INFORMATION: /desc = "Primer DA22"
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:
CATAACTGGA AATCGCCCGG GAACAGTTAC G 31

15

(2) INFORMATION FOR SEQ ID NO: 43:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: other nucleic acid
(ix) FEATURE:
(A) NAME/ KEY: misc-feature:
(B) OTHER INFORMATION: /desc = "Primer DA19"
(ix) FEATURE:
(A) NAME/KEY: misc-feature
(B) LOCATION: 12
(D): OTHER INFORMATION: /Note:W= mixture of A and T
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43

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CTGGAAATAA AWCCGGAACA GTTACG 36

35

2) INFORMATION FOR SEQ ID NO: 44:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: other nucleic acid
(ix) FEATURE:
(A) NAME/KEY: misc-feature:
(B) OTHER INFORMATION: /desc = "Primer DA23"
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:
GGAAATAAAC CAGGACCCGT TACGATCAAT GC 32

40

45

2) INFORMATION FOR SEQ ID NO: 45:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: other nucleic acid
(ix) FEATURE:

50

55

32

(A) NAME/KEY: misc-feature:
 (B) OTHER INFORMATION: /desc = "Primer DA32"
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:
 GAGGCTTGGA CTAGGTTTGA TTTTCCAG

28

5

2) INFORMATION FOR SEQ ID NO: 46:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs

(B) TYPE: nucleic acid

10

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(ix) FEATURE:

(A) NAME/KEY: misc-feature:

15

(B) OTHER INFORMATION: /desc = "Primer DA31"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

GCTGAATTTT GCGCAATGA TTTAGGTGCC

30

2) INFORMATION FOR SEQ ID NO: 47:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 34 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

25

(ii) MOLECULE TYPE: other nucleic acid

(ix) FEATURE:

(A) NAME/KEY: misc-feature:

(B) OTHER INFORMATION: /desc = "Primer bm4"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

30

GTGTTTGACG TCCCGCTTCA TGAGAATTTA CAGG

34

2) INFORMATION FOR SEQ ID NO: 48:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 34 base pairs

35

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(ix) FEATURE:

40

(A) NAME/KEY: misc-feature:

(B) OTHER INFORMATION: /desc = "Primer bm5"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

GTGTTTGACG TCCCGCTTCA TAAGAATTTA CAGG

34

2) INFORMATION FOR SEQ ID NO: 49:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 34 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

50

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(ix) FEATURE:

(A) NAME/KEY: misc-feature:

(B) OTHER INFORMATION: /desc = "Primer bm6"

33

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:
GTGTTTGACG TCCCGCTTCA TGCCAATTTA CAGG

34

2) INFORMATION FOR SEQ ID NO: 50:

5 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 32 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: other nucleic acid

(ix) FEATURE:

(A) NAME/KEY: misc-feature:

(B) OTHER INFORMATION: /desc = "Primer bm8"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

15 AGGGAATCCG GATACCCTGA GGTTCCTAC GG

32

2) INFORMATION FOR SEQ ID NO: 51:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 34 base pairs

20 (B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(ix) FEATURE:

25 (A) NAME/KEY: misc-feature:

(B) OTHER INFORMATION: /desc = "Primer bm11"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

GATGTGGTTT TGGATCATAA GGCCGGCGCT GATG

34

30 2) INFORMATION FOR SEQ ID NO: 52

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

35 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(ix) FEATURE:

(A) NAME/KEY: misc-feature:

(B) OTHER INFORMATION: /desc = "Primer p1"

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

CTGTTATTAA TGCCGCCAAA CC

22

2) INFORMATION FOR SEQ ID NO: 53:

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 24 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

50 (ix) FEATURE:

(A) NAME/KEY: misc-feature:

(B) OTHER INFORMATION: /desc = "Primer p2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

34

GGAAAAGAAA TGTTTACGGT TGCG

24

2) INFORMATION FOR SEQ ID NO: 54:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

10 (ix) FEATURE:

(A) NAME/KEY: misc-feature:

(B) OTHER INFORMATION: /desc = "Primer p3"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

GAAATGAAGC GGAACATCAA ACACG

25

15

2) INFORMATION FOR SEQ ID NO: 55:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(ix) FEATURE:

(A) NAME/KEY: misc-feature:

25 (B) OTHER INFORMATION: /desc = "Primer p4"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

GTATGATTTA GGAGAATTCC

20

INTERNATIONAL SEARCH REPORT

International application No.

PCT/DK 98/00471

A. CLASSIFICATION OF SUBJECT MATTER

IPC6: C12N 9/28, C11D 3/386

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC6: C12N, C11D

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

SE,DK,FI,NO classes as above

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

WPI, PAJ, BIOSIS, CA

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
P,X	WO 9741213 A1 (NOVO NORDISK A/S), 6 November 1997 (06.11.97) --	1-39
X	WO 9623874 A1 (NOVO NORDISK A/S), 8 August 1996 (08.08.96), See abstract, page 34 and claim 48 --	1-39
X	WO 9623873 A1 (NOVO NORDISK A/S), 8 August 1996 (08.08.96), See page 6, line 9-15, ex 4 and 5, page 75-77 --	1-39
X	WO 9100353 A2 (GIST-BROCADES N.V.), 10 January 1991 (10.01.91), page 4, line 16, claim 3 --	1-39

☒ Further documents are listed in the continuation of Box C.☒ See patent family annex.

* Special categories of cited documents:

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier document but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance: the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance: the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

"&" document member of the same patent family

Date of the actual completion of the international search

8 February 1999

Date of mailing of the international search report

16-02-1999

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 Swedish Patent Office
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INTERNATIONAL SEARCH REPORT

International application No.

PCT/DK 98/00471

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 9535382 A2 (GIST-BROCADES B.V.), 28 December 1995 (28.12.95), See abstract and claims --	1-39
A	WO 9510603 A1 (NOVO NORDISK A/S), 20 April 1995 (20.04.95) -- -----	1-39

INTERNATIONAL SEARCH REPORT

International application No.

PCT/DK 98/00471

Box I Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of Item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

The claimed inventions relate to variants of a parent Termamyl-like alpha-amylase.

A large number of mutations or combinations of mutations are suggested, which give

- a) improved pH stability at a pH from 8 to 10.5 and/or
- b) improved Ca²⁺ stability at pH 8 to 10.5 and/or
- c) increased specific activity at temperatures from 10 to 60C.

Mutations of Termamyl-like alpha-amylases are well-known in the art, see e.g. WO 96/23874.

No common theory for all the mutations are suggested in the present application. Therefore no "special technical feature" that makes a contribution to the prior art, as demanded in PCT rule 13.2, has been found.

The application claims a large number of inventions, in spite of this all inventions have been searched.

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☒ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

☐

The additional search fees were accompanied by the applicant's protest.

☐

No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

Information on patent family members

21/12/98

International application No.

PCT/DK 98/00471

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
WO 9741213 A1	06/11/97	AU 2692897 A	19/11/97
WO 9623874 A1	08/08/96	AU 4483496 A BR 9607013 A CA 2211316 A CN 1172501 A EP 0808363 A	21/08/96 28/10/97 08/08/96 04/02/98 26/11/97
WO 9623873 A1	08/08/96	AU 4483396 A BR 9607735 A CA 2211405 A CN 1172500 A EP 0815208 A	21/08/96 14/07/98 08/08/96 04/02/98 07/01/98
WO 9100353 A2	10/01/91	AT 166922 T AU 638263 B AU 5953890 A BG 61081 B CA 2030554 A CN 1050220 A DE 69032360 D,T EP 0410498 A,B SE 0410498 T3 ES 2117625 T FI 910907 D JP 4500756 T PT 94560 A,B US 5364782 A	15/06/98 24/06/93 17/01/91 31/10/96 30/12/90 27/03/91 03/12/98 30/01/91 16/08/98 00/00/00 13/02/92 08/02/91 15/11/94
WO 9535382 A2	28/12/95	AU 685638 B AU 2524795 A EP 0772684 A	22/01/98 15/01/96 14/05/97
WO 9510603 A1	20/04/95	AU 7807494 A BR 9407767 A CA 2173329 A CN 1134725 A EP 0722490 A FI 961524 A JP 9503916 T US 5753460 A US 5801043 A	04/05/95 18/03/97 20/04/95 30/10/96 24/07/96 30/05/96 22/04/97 19/05/98 01/09/98